

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 129485

TO: Mary Mosher

Location: REM/3D25/3C18

**Art Unit: 1648** 

Monday, August 23, 2004

Case Serial Number: 09/851410

From: Toby Port

**Location: Biotech-Chem Library** 

**REM-1A59** 

Phone: (571) 272-2523 toby.port@uspto.gov

## Search Notes

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## STIC-Biotech/ChemLib

1.09485

From:

Mosher, Mary

Sent:

Tuesday, August 10, 2004 8:17 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search 09/851410

Please translate & search AA encoded by:
nt 5147-7129 of SEQ 6
nt 5117-7096 of SEQ 10
And search SEQ 8.
Please do regular search, oligo search for the seq 6 & 10 translation products, and interference search. Thanks.

Mary Mosher AU 1648 571-272-0906 Office Rem 3D25 Mail Rem 3C18

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:

Online Time:\_\_\_

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Type of Search
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Structure: #\_\_\_\_\_\_\_
Bibliographic:
Litigation:
Patent Family:
Other:

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Vendors and cost where applicable
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August 21, 2004, 08:42:47; Search time 7642.28 Seconds (without alignments) 11246.543 Million cell updates/sec
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SUMMARIES

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Reyes,G.R., Bradley,D.W., Twu,J.-S.,
Krawczynski,K.Z. and Yarbough,P.O.
Hepatitis B virus vaccine and method
Patent: US 6455492-A 1 24-SEP-2002;
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                                                                                                                                                                                                                                                                                     GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG
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 GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                                                                                                                                                                      CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
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CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG

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Unknown. Unclassified

Unknown

Qy 1981 TAG 1983         Db 2026 TAG 2028		ORGANISM Unknown.  Unclassified.  REFERENCE 1 (bases 1 to 7195)  AUTHORS Reyes, G.R., Yarbough, P.O., Bradley, D.W., Krawczynski, K.Z., Tam, A.W. and Fry, K.E.  TITLE DNA sequences of enterically transmitted non-A/non-B hepatitis JOURNAL Patent: US 6229005-A 6 08-MAY-2001; FRATIBES	ce 1.7195, correction of the c	vative 0; Mismatches 0; Indels 0; Gaps cggcctartrigcrgcrccrcargrrrrgccrargcrccgcgcca	Oy   CCGCCCGGTCAGCCGTCTGGCCGCCGTGGCCGGCGCGGTGGT 120	Db 5267 TTCTGGGGTGACGGGTTGATTCTCAGCCTTGCGAATCCCTATATTCATCAACAAC 5326  Qy 181 CCCTTGGCCCCGGATGTCGCGGGGGGGGGGGGGGGGGGG	QY         241 CGACCACTCGGCTGACGGGCCCAGGGCCCCGCGGTGGCGTGGTGGT           1	Db 5447 AGACCTACACAGGCGGCGCGCTAACCGCGGTCGCTCCGGCCATGACCCCG 5506  Qy 361 CCAGTGCCTGATGTCGACTCCCGGGGCCCATGACCTATCAACCA 420	Db 5507 CCAGTGCCTGATGTCCGCGGGGCCCATCTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG	Db 5567 TCTCCCCTTACCTCTCCGGGCGCGCACCGGCTAACCTGGTTCTTAAGCCGCCCCTCTT 5626  Qy 481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATAAAAGGCCACGGAAGCTTCT 540  Db 6607 ACTCCCTTTTACCCCTTCAGGACGCACCAATAAAAAAAACGCCACGGAAGCTTCT 5686	541 AATTATGCCCAGTACCGGGTTGCCCGCCACAATCCGTTACCGCCCGC	
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Db 6827 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCT 6886  Qy 1741 ATTTCCACTTACACCACTAGCCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 1800  6887 ATTTCCACTTACACCACTGCGTGGTCCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 6946  Qy 1801 TTAGCCCCCACTCTGCGCTAGCATTGCTTGAGATACCTTGGGTTGCCGTT 6946  Db 6947 TTAGCCCCCACTCTGCGCTAGCATTGCTTGAGATACCTTGGACTGCCGGCCC 1860  1861 CATACTTTTGATGATTTCTGCCCAGTGCTTGAGATACCTTGGACTGCCTGC	RESULT 8 AR207633 LOCUS DECUS DECUS DESTINITION Sequence 6 from patent US 6379891. ACCESSION AR207633.1 GI:21507438 KEYWORDS COURCE ORGANISM Unclassified. REFERENCE TITLE AUTHORS AUT	ORIGIN	121 TTCTGGGGTGACCGGGTTGATTCTCGCAATCCCCTATATTCATCCAACCAA
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RVDSQPFALPAVAPPAHDTPVPAPAGGGFRYRQPARPLGSAMFDQAQRPAVASRRRP
TTAGGAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPL
SPLIPLOBGTNTHINATTEANYAQYRVARATTRYRPLVPNAVGGYAISISFWPOTTT
FTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV
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DQLLVBNAAGHRVAISTYTTSGLGAGFVSISAVAVLACHSSALLEDTLDSTPARHTED
DFCPECRPLGLQGCAFQSTVAELKKWVGKTREL"
                                                                                                                                                     LGUKTERTSTOOGAULETNOEPERINISEDAGGSTWAAGSESLTYAAGSAGLEGERTYAAG
GLOHRAVFACOVSPRSAPGGTAFCSALYRRNERAOGHSLIGNUMFIPEGILGLFAPF
SPGHVWESANPFGGESTTRTWSEVORANSSPARPLIGNUMFIPEGILGLFAPF
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PRILANEMPERANFPETGLTTEDVATANIALISEDSATDVGRACAGGRVTPGYVOYOF
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DAFDDTVFSAAVAAAKASMVPENDFSEFDSTQNNFSLGLECAIMEECGMPQMLIRLYH
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PADVCELIRGAYPMIQTTSRVLRSLEWGEPAVGQKLVFTQAAKPANPGSVTVHEAQGA
TYTETTIIATADARGLIQSSRAHAIVALTRHTEKCVIIDAPGLLREVGISDAIVNNFF
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SYLCSETKOGSPGAAVLIAGGCGLKLKVDFRPIGLYAGYVVAPGLGALPDVVRFAGRLT
EKNWGPGPERARQLEAVSDFLRKLTNVAQMCVDVVSRVYGVSPGLVHNLIGMLQAVA
DGKAHPTESVKPVLDLTNSILCRVE"
VHRCFLRPVGRDVQRWYTAPTRGPAANCRRSALRGLPAADRTYCLDGFSGCNFPAETG
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VIYYEGDTSACYNHDVSLLRSWI RTTXYTGDHFLVI IRYRAIGGHFVLLLTAFBFSPB
PYVPYPRSTEVYVRSIFGPGGTPSLFPTSCSTKSTFHAVPAHIWDRLMLFGATLDDQA
                                                                             FCCSRLMTYLRGISYKVTVGTLVANEGWNASEDALTAVITAAYLTICHQRYLRTQAIS
                                                                                              KGMRRLEREHAQKFITRLYSWLFEKSGRDYIPGRQLEFYAQCRRWLSAĞFHLDPRULV
FDESAPCHCRTAIRKALSKFCCFMKWLGQECTCFLQPAEGAVGDQGHDNEAYEGSDVD
PAESAISDISGSYVVPGTALQPLYQALDLPAEIVARAGRLTATVKVSQVDGRIDCETL
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/mol type="genomic DNA"
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Takeda,N., Ri,T. and Miyamura,T.

HEPATITIS E VIRUS HOLLOW PRRITCLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR.

L PATENT: JP 1998234383-A 3 08-SEP-1998;

DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
OS HEDALILIS E VILUS
PD 08-SEP-1998
PP 28-FEB-1997
PP 1997062445
PI TAKEDA NAOKAZU, RI TERNSEI, MIYAMURA TATSUO
PC CI2N15/09,C07K14/08,C12N5/10,C12P21/02;
                                                                                                                                                     GACCAGTCCACTTATGGCTCTTCGACTGCCCAGTTTATGTTTCTGACTCTGTGACTTG
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               CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
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DQLUVENAAGHRVALSTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPACAHTFD
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TTAGAAPLTAVAPAHDTPPVPDVDSRAAIILRRQYNLSTSPLTSSVATGTNILVLYAAPL
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MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
ADGTAELTTTAATRFMKDLYFTSTNGVGBIGRGIALTLFNLADTLLGGLPTELISSAG
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ILINLMQPRQLVFRPEVFWNHPIQRVIHNELELYCRARSGRCLEIGAHPRSINDNPNV
VHRCFLLPVGRDVQRWYTAPTRGPAANCRRSALRGLPAVDRTYCLDGFSGCNFPAETG
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VYTRGOTTSGOTNHDVSDLRSWTRTTYKTGDHPUYLERVRATGGHFVLLTAAPRESEM
PYVPYPRSTEVYWR 11 EGPGGTPSLFPTSGSTKSTFHAVPAHTWDRALFGATLDDQA
FCCSRLMTYLRGISYKVTVGTLVANEGWNASEDALTAVITAAYLTICHQRYLRTQAIS
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|/translation="WINMANSFAAPMGSRPCDLGLFCCCSSCFCLCCPRHRPVSRLAAVV
|GAAAVPAVVSGVTGLILSFSQSPIFIQPTFSPPMSPLRPGLDLVFANQPDHSAPLGV
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       Tokyo 173, Japan (Tel:81-3-3972-8111
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'db_xref="GI:221705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hepatitis E 'mol type="genomic RNA" /isolate="HEVNE8L"
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Location/Qualifiers
                                                                                                                                                     Ist Department of Pathology
Nihon University School of
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/product="ORF1"
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/product="ORF3"
                                          Fax:81-3-3972-8830)
Submitted (23-Jan-1992)
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                                                                                                                  Joshikazu Uchida
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Itabashi-ku, To
Japan
Phone: 81-3-39
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MICHIGSPWASYTNTPYTGALGLIDPALELBERNITPGNYNTWRYSRYSTAHRILRS
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DQLLVENAGHRVATSLGAGFYSIGNAVAVFRHSALALLEDTLDYFRAHFFD
DFCPECRRLGLGGGAFQSTVARLYGKKKKKTREL"
                                                                                                        linear VRL 24-JUL-1999 gene, complete cds.
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RVDSQPFATIOTYPFWPRPAPDVTAAAGAGRRIROPARPLGSARNDOAGRARAGRRRP
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SPLIPLOGGTWYHIMATEASNYAQYRVARATIRYRPLVPNAVGSYAISISFWPQTTT
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Arankalle, V.A., Paranjape, S., Emerson, S.U.,
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Arankalle, V.A., Paranjape, S., Emerson, S.U.,
alimbe, A.M.
                                                                                                                                                                                                                                          Hepatitis E virus
Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no
E-like viruses.
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                                                                                                        AF124407 1983 bp RNA
Hepatitis E virus isolate AKL-90 ORF-2
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llarity 97.8%; Pred. No. 0;
Conservative 0; Mismatches
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/mol_type="genomic RNA"
/isolate="AKL-90"
/db_xref="taxon:12461"
/country="India"
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/db_xref="GI:5579230"
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/product="ORF-2"
                                                                                                                                                                                          AF124407.1 GI:5579229
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PELLAARKFEARRFTETLI ITEDVARTANLA I ELDSATDVGRACAGGRYTPGTVQYQ
TAGVPGSGKSRS ITQADVDVVVVPTRELRNAWRRGFAAFTPHTAARVTGGRRVVIDB
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PADVCELIRGAYPMIQTTSRVLRSLFWGEPAVGQKLVFTQAGKAANPGSVTVHEAQGA
TYTETTIIATADARGLIQSSRAHAIVALTRHTEKCVIIDAPGLLREVGISDAIVNNFF
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RPTBSPAPSRPFSVLRANDVLWLSLTAAEYDGSTYGSSTGPVYVSDSVTLVNVATGAQ
AVARSLDWTKVTLDGRPLSTIQQYSKTPFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
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FCCSRLMTYLRGISYKVTVGTLVANEGWNASEDALTAVITAAYLTGHQRYLRTQAIS
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/translation="MNNMSFAAPTGSRSCALGLFCCCSSCFCLCCPRHRPVSRLAAVV
GGAAAVPAVVSGVTGLILSPSQSPIFIQPTPSPPMSPLRPGLDLVFANPPDHSAPLGV
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MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
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DFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"
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NASHSDVRDSLARFIPAIGPVQVTTCELCELVEAMVEKGQDGSAVLELDLCNRDVSRI
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                                                                                                                              experimentally infected
                                                                                                                                                                                                    /note="encodes cysteine protease, RNA helicase and MNA-dependent RNA polymerase, ORF1" (codon start=1 /codon start=1 polyprotein"
                                                                                                                           /note="isolated from the bile of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="immunogenic protein"
/protein_id="AAC97187.1"
E virus"
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                     /mol_type="genomic RNA"
/strain="TK15/92"
                                                                      xref="taxon:12461"
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organism="Hepatitis"
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                                                                                                   country="Nepal"
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/note="ORF2"
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                                              Gaps
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    Score 1896.6;
Pred. No. 0;
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95.6%;
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                  CTCACCACCACGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
                                                                                 GTTGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
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                                                       GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                                                           <u> GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC</u>
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AF185822 7143 bp RNA linear VRL 14-JUN-2001 Hepatitis E virus nonstructural polyprotein gene, partial cds;

RESULT 15 AF185822 LOCUS DEFINITION

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APGVSPRSAPGEVTÄPCSALYRFNREAQRHSLTGOLMPFPEGLIGLFAPFSPGHVWES
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EANLFTRAALTITEDATVORTATALTATTTYCPTGVPTGAVQYCYGTAGVPGGG
KSRSITQADVDVVVVPTRELRNAMRRRGFAAFTPHTAARVTGGRRVVIDEAFSILPPHL
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|db_xref="GI:10336833"
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VGRDVQRWYTAPTRGPAANCRRSALRGLPAADRTYCFDGFSGCSFPAETGIALYSLHD
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TRVVVRSI ECPEGTPSLEPTGCSTKEPTAVPRHIWDRIME GANTLDOAPRCCSRIMT
YLGII SYKVTVGTI VANEGWVASEDALTAVITAAYLITCHQRYLRTQAI SKGMRELER
EHAQKE ITRLYSWLFEKSGRDYI PGRQLEFYAQCRRWLSAGFHLDPRVI VPDESAPCH
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ISGSYVVPGAALQPLYQALDLPAEIVARAGRLTATVKVSQVDGRIDCETLLGNKTFRT
SFVDGAVLETNGPERHNLSFDASQSTWAAGPFSLTYAASAAGLEVRYVAAGLDHRAVF
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RGAYPMIQTTSRVLRSLFWGEPAVGQKLVFTQAAKAANPGSVTVHEAQGATYTETTII
ATADARGLIQSSRAHAIVALTRHTEKCVIIDAPGLLREVGISDAIVNNFFLAGGEIGH
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LYAPOBLITTCDSVVTFELITDTHGKMAAPSQREAVLSTLVGRYGRRITKTVNASHSDVR
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KFTTGETTAHGKVGGGISANSKTFCALFGPWFRAIEKALLALLPQGVFYGDAFDDTVF
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RQSPGAAVLIAGCGLKLKVDFRPIGLYAGVVVAPGLGALPDVVRFAGRLTEKNWGPGP
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Caudill,J.D., Snellings,N.J., Begot,L., Innis,B.L., Longer,C.F. and
                                                                                                                                                                                                                                                                                                        1 (bases 1 to 7143)
van Cuyck-Gandrey, Zhang, H.Y., Tsarev, S.A., Warren, R.L.,
Caudill, J.D., Snellings, N.J., Begot, L., Innis, B.L. and Longer, C.F.
Short report: phylogenetically distinct hepatitis E viruses in
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                                                                                                                                  Hepatitis E virus
Hepatitis E virus
Viruses; BSRNA positive-strand viruses, no DNA stage; Hepatitis
E-like viruses.
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Direct Submission
Submitted (13-SEP-1999) Agents Transmissibles, CRSSA, 24 Ave.
Maquis du Gresivausan, BP 87, La Tronche 38702, France
Location/Qualifiers
protein gene, complete cds; and unknown gene.
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/note="ORF3"
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Search completed: August 21, 2004, 15:14:59 Job time: 7653.28 secs

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Minimum Maximum Database

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Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody; diagnosis; HEV; ds.
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AAV66322
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AAA99260
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89US-00336672.
89US-00367486.
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92US-00876941.
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    (first entry)
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/product=
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17-JAN-1992;
20-APR-1992;
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11-APR-1989;
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13-OCT-1989;
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  ' Search time 765.579 Seconds
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Compugen Ltd.
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            GenCore version (c) 1993 - 2004
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Listing first 45 summaries
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                                                                                         A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence encodes the protein from the open reading frame, ORP2, from HEV Burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines
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100.0%; Score 1983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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P-PSDB; AAR96089.
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13-OCT-1995;
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Immunogenic hepatitis B virus (HEV) peptides are selected from the ORF1, ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to prevent infection by HEV. The antibodies can neutralise and block HEV infection and can be used to prevent or treat HEV infection. The peptides and antibodies can also be used as diagnostic reagents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
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Best Local Similarity
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                                                       20-APR-1992;
                                         17-JAN-1992
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The present sequence represents the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis virus (HEV)). The specification describes an isolated protein which is specifically immunoractive with antibodies present in individual is infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF) sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-2003 to correct OR field.)
          diagnosis or vaccine production
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/note= " encodes AAW80197"
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5106. .5477
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P-PSDB; AAW80196, AAW80197, AAW80198
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00505888.
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
05-APR-1990;
25-JUL-1994;
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23-DEC-1998
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Enterically transmitted nonA/nonB hepatitis virus; identification; HEV; ET-NANB; detection; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the sequence of the Burmese isolate of enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV), detecting ET-NANB in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in vaccines. (Updated on 25-MAR-2003 to correct PF field.)
7007 CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC
                                                          CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG
                                   CAGICIACIGICGCIGAGCIICAGCGCCTIAAGAIGAAGGIGGGIAAAACTCGGGAGIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yarbough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E virus DNA - useful for e.g. virus detection and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;
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Ouery Match  100.0%; Score 1983; DB 2; Length 7195;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps  1 ATGCGCCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCCGGCCA 60	DD 5207 CCGCCCGGTCTGGCCGCCGCGCGGGGGGGGGGGGGGGG	241 CGACCACTCGGCTCCGCTTGGCGTGAGCCCAGCGCCCCCCGCTTGCTCTCACTCGT 30  241 CGACCACTCGGCTCGGCTGAGCGTGAGCCCAGCGCCCGCTTGCTT	301 AGACCTACCACAGCTGGGGCCGCGCTAACCGCGGTCGGCCCATGACACCCCGG 360	DD SSO/ CCAGIGCCIGATGICGACGCGGGGGCCAICIIGCGCCGGCAGATAACCTAICAACA 5566  QY 421 TCTCCCCTTACCTCTTCCGTGGCCACCAGCACTAACCTGGTTCTTTAIGCCGCCCCTCT 480	AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540	QY         541 AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCTGGTCCCCAAT 600           DD         5687 AATTATGCCCAGTACCGGTGCCACAAATCCGTTACCGCCGCTGGTCCCCAAT 5746	QY         601 GCTGTCGGCGGTTACGCCATCTCCATCTCGCCACAGACCACCACCACCACGGCG         660           Db         5747 GCTGTCGGCGGTTACGCCATCTCCATCTCTGGCCACAGACCACCACCCCGACG         5806	OY 661 TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCGGCATA 720	OY 721 GCCTCTGAGCTTGTGATCCCAAGTGAGGCCTACACTATCGTAACCAAGGCTGGGGCTCC 780	QY 781 GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840	QY 841 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 900	OY         901 GACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC 960           Db         6047 GACTTTGCCTTGAGCTTGAGTTTCGCAACCTTACCCCGGTAACACCAATACGCGGGTC 6106	OY 961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGACGGA

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                                                                                  Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein; immunological; diagnosis; hepatitis; infection; identification; detection; immunoreactive; hepatotropic; antiinflammatory; virucide; vaccine; antiviral; antiogenic; antibody; antigen; ds.
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P-PSDB; AAB24119, AAB24120, AAB24121.
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89US-0033672.
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Krawczynski KZ,

Bradley DW,

Yarbough PO,

SERVICES

TECHNOLOGIES INC

DEPT HEALTH & HUMAN

88US-00208997. 89US-00336672. 89US-00420921. 90US-00505888. 91US-00681078.

98US-00128275

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                                                                                                                                 The invention relates to an isolated DNA comprising the genome of an enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also referred as HEV). The DNA sequences or their fragments are useful in preparing ET-NANB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The present sequence represents a ET-NANB viral DNA sequence from HEV-Burma strain
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New DNA sequences of enterically transmitted non-A/non-B (ET-NANB) hepatitis viral agent, useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
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HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral; ET-NANB; infection; vaccine; ds.

Hepatitis E virus.

ET-NANB viral DNA sequence from HEV-Burma strain.

(first entry)

23-JUL-2001

AAF83495

BP

AAF83495 standard; DNA; 7195

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ive 0; Mismatches
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P-PSDB; AAO15698, AAO15699, AAO15700.
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05-APR-1990;
15-APR-1991;
25-JUL-1994;
07-JUN-1995;
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US6379891-B1
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16-JUN-1989;
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                                                                                                                                                                                            The invention relates to a protein derived from an enterically transmitted non-A/non-B viral heparitis agent. The viral proteins are useful for detecting infection by the enterically transmitted non-A/non-B viral agent. The proteins are also useful for producing vaccines for immunising an individual against HEV heparitis viral agent. The DNA fragments are useful for identifying and sequencing the entire viral agent and for assaying the viral agent in an infected sample. The present sequence is used in the exemplification of the
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             Bradley
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Best Local Similarity 99.8%;
Matches 1980; Conservative
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                                                                                                                             CTCCGCGGGTAAGCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT
                                                                                                                                               CTCCGCGGTAAGCTCTTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT
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              GITAATGITGCGACCGGCGCGCAGGCCGITGCCCGGTCGCTCGATTGGACCAAGGTCACA
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89US-00336672.
89US-00420921.
90US-0056888.
91US-00681078.
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
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05-APR-1991
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6947 TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCC
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         TTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC
                                                                                                                             CATACITITGAIGAIITCTGCCCAGAGIGCCGCCCCCTIGGCCTTCAGGGCTGCGCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New viral proteins from non A-non-B hepatitis agent - used to treat prevent enterically-transmitted non-A non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterically transmitted non-A, non-B hepatitis virus; hepatitis C; E.coli strain BB4; ATCC deposit number 67117; Burma; ss.
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5147. .7129
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P-PSDB; AAR14618, AAR14619, AAR14620.
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16-JAN-1992
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cynomolgus monkeys infected with the Burma strain of ET-NANB. Both strands of ET1.1 were sequenced. Identity of the sequence with sequences in etiologic agents has been confirmed by locating a similar sequence in a viral strain isolated in Burma. T(U sequence of the Burma strain is given here. See AAQ14410 for ET1.1. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA
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This sequence encodes a Hepatitis B viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HBV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HBV than
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of HEV
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encoding it - useful for more accurate detection immuno-assays and nucleic acid hybridisation.
                                                                                                                                                                  Score 1949.4;
Pred. No. 0;
                                                                                                                                                                               Pred. No. 0;
0; Mismatches
                                    Disclosure; Page 27-29; 29pp; Japanese
                                                                                                                                                                    Query Match
Best Local Similarity 98.9%;
Matches 1962; Conservative
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  GACCAGICCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG
                                                                                                   GITAATGTTGCGACCGGCGCGCGCGTTGCCCCGGTCGCTCGATTGGACCAAGGTCACA
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                                                                                                                                                                                                              (revised)
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          CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
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Polypeptide fragments of hepatitis B virus (HEV) for va and diagnosis in preventing and treating HEV infection. Example 1; Page 82-83; 91pp; Chinese. ŝ 2000CN-00130634 ge ဥ TANG Ξ WPI; 2002-427096/45. SHENG ٦,

invention relates to novel n-mer polypeptides comprising amino acids of ORF-2 of HEV where n = 2-180. The polypeptides of the invention have virucide activity. The polypeptide of HEV, its fragments, and chimeric proteins, are useful for vaccine compositions and diagnosis in preventing and treating HEV infection by immunisation, which may also be applied in the diagnosis of HEV infection

T; 0 U; 0 Other; Sequence 1990 BP; 348 A; 666 C; 481 G; 495

120 120 180 240 240 300 300 360 9 9 CCCTTCGCCCCCGATGTCACCGCTGCGGGGCTGGACCTCGTGTTCGCCAACCCGCC ATGCGCCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGGCGCA CCGCCCGGTCAGCCGTCTGGCCGCCGTCGTGGGCGGCGCGCAGCGGCGGTTCCGGCGGTGGT CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCC CACCACTCGGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGT AGACCTACCACAGCTGGGGCCGCCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCG Gaps Length 1990; 0; Indels . 9 111; 四 Score 1805.4; Pred. No. 0; 0; Mismatches 91.0**%**; 94.4%; Best\_Local Similarity 94.4 Matches 1872; Conservative 121 61 61 121 181 181 241 Query Match 241 301 δ qa a δ 8 A g g  $\delta$ qq qq ð ò

360 420 420 480 480 540 540 009 600 099 099 720 TCTCCCCTTACTTCTTCCGTGCCACCGGTACAAACTTGGTTCTATACGCCGCTCCTTT TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA CCAGTGCCTGATGTCGACTCCCGCGGCGCCATCTTGCGCCGGCAGTATAACCTATCAACA TCTCCCCTTACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCTCTT AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCACCGACG 301 541 361 361 421 421 481 481 541 601 601 199

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Oy 1801 TTAGCCCCCCACTTGCGCTAGGATACCTTGAACACTACCTGGCCGCC 1860

Db 1801 TTAGCCCCCCACTCGCGCTAGCATTGCTTGAAGATACCATGAACTACCTGCCCGCGC 1860

Oy 1861 CATACTTTGATGATTTCTGCCCAGAGTGCCGCCCTTGAGCTTACCTTGAACTTC 1920

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Oy 1921 CAGTCTACTGTCGCTGAGCTTCAGGCCTTAAGATGAAGTGGGTTAAAACTCGGGAGTTT 1920

Db 1921 CAGTCTACTGTCGCTGAGCTTCAGGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTT 1980

Oy 1981 TAG 1983

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Search completed: August 21, 2004, 11:00:11
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AL578906 AL578906
BX335523 BX335523
BX403654 BX403654
                                                                  August 21, 2004, 10:14:02; Search time 5116.87 Seconds (without alignments) 11572.836 Million cell updates/sec
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			CNSO091P Drosophila mei BACR19D16 of 11y, genomic AL053013, AL053013,1 G GSS. Drosophila mei Drosophila mei Eukaryota; Met Neoptera; End Neoptera; End Neoptera; End Driect Submiss Submitted (02- BP 191 91006 F Web: www.gq Determination The BDGP is contained to the BDGP i
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen.FRATURES Location/Qualifiers Contact : Feng Liang Email
: fliang@lifetech.com URL : http://fulllength.invitrogen.com/
InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID :
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(Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

(Oppublished (2001)
                                                                                                                                                                                                     /cell type="HELA CELLS COT 25-NORMALIZED"
/cell line="HELA"
/clone lib="HELA"
/clone lib="HOLM"
/note="Ist trand cDNA was primed with a NotI-oligo(dT)
/note="Ist trand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK005AAl0QPl.
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clone CSODIO1SYN12 3-PRIME, mRNA sequence.
BX335523. GI:30312422
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Similarity 39.7%; Pred. No. 0.00012;
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/organism="Homo sapiens"
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  Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BOGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP from the and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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1. (bases 1 to 1201)

1.i., W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12943429.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
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AL578906
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 584.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODKO05AA10QPl&cluster=584.f. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 CCGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        810 YMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGSSSTNGMBGTSSACSSSSS
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                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACR19D16"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.0001;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548
                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com I
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                              Length 1201;
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Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                             Score 63.6; DB 13;
Pred. No. 0.00083;
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Genoscope - Centre National de Sequencage
                  organism="Homo sapiens"
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                                                   xref="taxon:9606"
                                                                 /clone="CS0DI015YN12"
                                  L type="mRNA"
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.r
Contact : Feng Liang Bmail: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO72CF03NPI.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1103;
Avenue Genoscope sequence ID : CLOBA007ZH12FP1
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 62.2; DB 13; 29.2%; Pred. No. 0.0017; Live 89; Mismatches 144;
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                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA007ZH12"
                       Location/Qualifiers
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BX360624.1 GI:30376452
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BX349688 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI063YK05 3-PRIME, mRNA sequence.
BX349688
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                                                                                                                                                                                                      CTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCTTCGCCCCCCGGATGTCACCG 202
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1 (bases 1 to 1057)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7092.r For
more information about this cluster, see
Http://www.genoscope.cns.fr
Ggi-bin/cluster.cgi?seq=CSOBAHO15ZB03NP1&cluster=7092.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAHO15ZB03NP1.
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                                                                                                                                               Gaps
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                                                                                                                                           0; Mismatches 327; Indels
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                                                                                 Score 60.2; DB 29
Pred. No. 0.0064;
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                                                                                 3.0%;
ilarity 37.2%;
Conservative
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BX349688/c
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An incegrated physical and genetic map of the nematode Pristionchus
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/mol_type="mRNA"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGTCAGCCGTCTGGCCGCCGTCGTGGGCGCGCAGCGGCGGTTCCGGCGGTGGTTTCT
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0
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenanustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
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/mol_type="genomic DNA"
/strain="California"
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Neodiplogasteridae; Pristionchus.
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nes 25; Conserv
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/clone="BACR11P16"
/clone_lib="RPCI-98"
/note="end : TET3"
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Cancer Genetics
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59; Conserv
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BX446579/c
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                  /tissue type="Placenta cor 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                              209
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                       CITCGCAATCCCCTATATTCATCCAACCAACCCTTCGCCCCCGATGTCACCGCTGCGGC
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Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                      3.0%; Score 60; DB 13; Length 1057; 32.1%; Pred. No. 0.0055; ive 77; Mismatches 181; Indels (
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            organism="Homo sapiens"
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                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                      /clone="CS0DI063YK05"
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Drosophila melanogaster
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Linvitrogen. This sequence belongs to sequence cluster 7325.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB002E710FP1&cluster=7325.f. Contact :
Feng Liang Email: fliangedlifetech.com VEL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBB002E710FP1.
at the Roswell Park Cancer Institute in Buffalo
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BX446579 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB002ZF10 3-PRIME, mRNA sequence.
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ilarity 19.9%; Pred. No. 0.0061;
Conservative 127; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:7227"
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UG/54612 1793 bp DNA linear GSS 24-OCT-2003
P050-1-D08.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSSSTSSTTSSTTGKGCSKGGSBSGGSSSSSGCGTYSSSTGGSGSSVSGSSGGSSBGSS
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                         Length 839;
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BARR10E16"
/clone lib="RRCI-98"
/note="end: TET3"
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                                                                                                                                                                                                                                                                                                                                         Score 59.2; DB 29;
Pred, No. 0.0076;
                                                                                                                                                                                                                                                                                                                                                                                       129;
                                                                                                                                                                                                                                                                                                                                                                                          65; Conservative 147; Mismatches
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Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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1. .1793
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CG754612.1 GI:37980282
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                                                                                                                               1. .839
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Determination of this BAC-and sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecokl digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                              /tissue type="NEUROBLASTOMA"
/cione lib="Homo sapiens NEUROBLASTOMA"
/cone lib="Homo sapiens NEUROBLASTOMA"
/note="Wector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI oligo(dT) primer of the prime end cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Beoptera; Endoptazoyata; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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llarity 36.0%; Pred. No. 0.0073;
Conservative 65; Mismatches 144;
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                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB002ZF10"
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                       library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Generieve Payan. It has been constructed in the vector pBeloBAC11.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Mismatches 207;
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                                                                                                                                                                                                                /organism="Drosophila mel
Mol type="genomic DNA"
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/clone=lib="DrosBAC"
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/note="end:SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly), genomic survey sequence.
AL066742
                                                                                                                                                                  Location/Qualifiers
http://www.edgp.ebi.ac.uk
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/clone="CaxOn."
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/clone="made and female"
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/dev stage="heads and internal organs combined"
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/clone lib="SHGC-CDA"
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/s' adaptor); Site_2: KhoI (3' linker primer); The mixed
organ cDAA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a 50 bp linker primer containing an oligo dT sequence
preceeded by a synthetic KhoI site. 5 prime adaptors were
used containing an EcoRl cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lacZ promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary olones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."
                                                                                   CA 94305-5329, USA
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      Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford,
Tel: 650 725 5954
Fax: 650 725 7739
Email: Kingsley@cmgm.stanford.edu
Plate: 90
                                                                                                                                                                                                                                                                /organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                               High quality sequence stop: 172.
Location/Qualifiers
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Unpublished (2003)
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1 (bases 1 to 1174)
Ringsley, D. M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R. M.
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                  please see http://www.fruitfily.org The BIGF Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BIGF from the isogenic strain y2; cn bw sp, the same strain used for the BIGF from the In and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or fillters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCA 170
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           For further information
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2.9%; Score 58; DB 29; Length 932;
Best Local Similarity 33.1%; Pred. No. 0.015;
Matches 120; Conservative 81; Mismatches 156; Indels
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         genome using these BACs.
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/lab_host="nH10B (phage-resistant)"
/lab_host="nH10B (phage-resistant)"
/clone_lib="NH1MGC_98"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2:
BcoRI; cDNA made by oligo-dT priming. Directionally
cloned into BcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California. Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imag.llnl.gov.c column: 06
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-870-985A-1
US-08-478-507-6
US-09-128-275A-6
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Maximum Match 100%
Listing first 45 summaries
                                        - nucleic search, using sw model
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Maximum DB seq length: 200000000
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APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Yarbough, Parrice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
CORRESPONDENCE ADDRESS:
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ORF-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IIAP PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENDTH: 1983 base pairs

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                     Genelabs Technologies, Inc
                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08240049B
Patent No. 5686239
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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TOPOLOGY: li
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STATE: CA
COUNTRY: US
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STREET: 50
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1 ANGOGGCCTGGGCCCATTTTTGTTGCTGCTCCTGARGTTTTTGCCTATGCTGCCGCCCCA 60 1 ANGOGGCCTGGGCCCATTTTTTTTTGTTGCTGCTCCTGCTGCCCCCCCC	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGACGGGACTGCCGAG 1020

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                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-UN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
             APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yazboud, Patrice D.
ITLE OF INVENTION: Hepatitis E Virus Vaccine
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE: INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE
                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1983;
100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                               CLASSIPCATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 367,486 FILING DATE: 16-JUN-1989 PRIOR APPLICATION DATE: APPLICATION NUMBER: US 336,672
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NO
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FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
Tam, Albert W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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STRANDEDNESS: doub]
TOPOLOGY: linear
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Best Local Simi
Matches 1983;
           APPLICANT:
APPLICANT:
                                                                                                                                                         COUNTRY:
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                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFRARE: PATCHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: 4600-0093.38
                                                                                                                                                                                                                                                                                                            PRIOR DATE: 1/-DAY 1592

PRIOR DATE: 1/-DAY 1592

APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921

FILING DATE: 13-OCTOBER-1989

PRIOR APPLICATION NUMBER: US 367,486

FILING DATE: 10-UNE-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

PRIOR APPLICATION NUMBER: US 208,997

FILING DATE: 17-UNE-1989

PRIOR APPLICATION NUMBER: US 208,997

FILING DATE: 17-UNE-1988

ATTORNEY/AGENT: INFORMATION:
NAME: SHOLTZ, CHARIES K.
                                                                                                                                         FILING DATE: 07-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
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TELEPRONE: (415) 324-0880
TELEPRAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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TOPOLOGY: lir
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GENERAL INFORMATION:
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Arawczynski, Krzysztof Z.
APPLICANT: ARAWCZYNSKi, Krzysztof Z.
ANWHER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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350 Cambridge Avenue, Suite 250
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
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301 AGACCTACCACAGCTGGGGCCGCCGAAACGGGGTCGCTCCGGCCCATGACACCCCG 360 		TACCTCTTCCGTGGCCACGGGACTAACCTGGTTCTTATGCCGCCCCCTCTT	TTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT	541 AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC	601 GCTGTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCGGACG 660 	661 TCCGTTGATATGAATTCAATAACCTCGACGATGTTCGTATTTTAGTCCAGCCCGGCATA 720 	721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780 	781 GTCGAGACTCTGGGGTGGCTGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840 	841 CATGGCTCACTGTAAATTCCTATACACCCTATACGGGGGGGG	901 GACTITIGCCTITGAGTITGGCAACCITACCCCGGTAACACCAATACGCGGGTC 960 	961 TCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020 	1021 CTCACCACCACGGCTGCTACCGGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080 	1081 GTCGGTGAGATCGCCGCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT 1140 	1141 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCGGCGGCTGTTCTACTCCCGTCCC 1200 	1201 GITGICTCAGCCAATGGCGAGCCGACTGITAAGTIGIATACAICTGIAGAGAAIGCTCAG 1260 	1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGGGTTATT 1320 	1321 CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC 1380 

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                            4600-0093.33
                                                                                                                          APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 38,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY AGENT INFORMATION:
                  FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
         US 822,335
                                                                                                                                                                                                                                              NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
STRANDEDMESS: double
TOPOLOGY: linear
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; INDIVIDUAL ISOLATE: ORF
US-07-876-941A-3
         APPLICATION NUMBER:
FILING DATE: 17-JAN
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                      Hepatitis E Virus (Burma strain)
ORF-2
                                                                                100.0%; Score 1983;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                Query Match
Best Local Similarity 100.
Matches 1983; Conservative
                    INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
    ORIGINAL SOURCE:
                                                  US-08-542-634-1
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APPLICANT: McAtee, C. Patrick
APPLICANT: Arbough, yifan
APPLICANT: Zhang, Yifan
TILB OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/542,634
FILING DATE:
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350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                    Sequence 1, Application US/08477292
Sequence 1, Application US/08477292
Patent No. 6221641
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas
APPLICANT: Yarbough, Patrick
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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ORF-2
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100.0%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                   SSEE: Cathleen M. Desjardins, M. F: 505 Penobscot Drive Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/327,952
APLING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G32P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
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TELEPHONE: (415)369-9500
TELEFAX: (415)368-07950
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
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EDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
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Best Local Similarity
Matches 1983; Conserv
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US-08-477-292-1
RESULT 6
US-08-477-292-1
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-7AN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 11-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 36,672
FILING DATE: 11-APPLIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-APPLIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-OUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0880
TELEFAX: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARATTERITICS:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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STRANDEDNESS: double
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llarity 100.0%;
Conservative 0;
     ; INDIVIDUAL ISOLATE:
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PCT-US95-13703-1
                                                            Query Match
Best Local Similarity
Matches 1983; Conserv
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CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG
                                                        CTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT
                                                                                                              TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9513703
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defilinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306-0850
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RADIAN, GALYR
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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PCT-US95-13703-1
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                                   GENERAL INFORMATION:

APPLICANT: Reyee, Gregory R.

APPLICANT: Twu, Or-Shin

APPLICANT: Twu, Or-Shin

APPLICANT: Tam, Albert W.

APPLICANT: Krawszynski, Krzysztof Z.

APPLICANT: Krawszynski, Krzysztof Z.

APPLICANT: Tam, Albert W.

APPLICANT: Tam, Albert W.

APPLICANT: Tam, Albert W.

APPLICANT: Trabough, Patrice D.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
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OPERATING SYSTEM: PC-DOS/NS-DOS
OSFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-7UN-1994
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INDIVIDUAL ISOLATE: BURMA SEQUENCE, FIGURE
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                           3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
PRIOR DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 420,921
PRIOR APPLICATION NUMBER: US 367,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-UNM-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
            Sequence 1, Application US/08259148A Patent No. 5741490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
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Matches 1983; Conservative
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CLASSIFICATION:
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                                                                                                                                             GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                                                                                                                  GTTGTCTCAGCCAATGGCCGAGCCGACTGTTAAGTTGTATACATCTGTAGAATGCTCAG
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                                                                                       CTCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTACTAGTACTAATGGT
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                                                                                                                                      AGACCTACCACAGCTGGGGCCGCGCCTAACCGCGGTCGCTCCGGCCCATGACACCCCCG 360
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                       226 CCCTTCGCCCCCCGATGTCACCGCTGCGGCCCGGGCTGGACCTCGTGTTCGCCAACCCGCC
                                                                                      CACCACTCGGCTCCGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGT
                                                                                                                                                            CCAGTGCCTGATGTCGACTCCCGCGGGGCCCATCTTGCGCCGGCAGTATAACCTATCAACA
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CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCC
                                                                  CGACCACTCGGCTCCGCTTGGCGTGACCAGGCCCCAGCGCCCCCGCCGTTGCCTCACGTCGT
                                                                                                                                                                                                         CCAGTGCCTGATGTCGACTCCCGCGCGCCATCTTGCGCCGGCAGTATAACCTATCAACA
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                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                  CURKENI AFPLICATION DATA:

PAPELICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 17-JAN-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 36,672
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
RESTSTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.38
TELEGOMENTICATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.38
       AUDKESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1983; 100.0%; Pred. No. 0;
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TELEFAX: (415) 324-0860
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 1983; Conservative
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STRANDEDNESS: double
                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PLICATION UNFBRE. US/07/876,941A
FILING DATE: 01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                             PULING DATE:

APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-JAN-1992
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 0.5-APRL-1990
FRICK APPLICATION NUMBER: US 420,921
FILING DATE: 1.0-APRL-1990
FRICK APPLICATION NUMBER: US 420,921
FILING DATE: 1.0-CYCOBER.1989
FRICK APPLICATION NUMBER: US 36,7486
FILING DATE: 1.0-AUNE-1989
FRICK APPLICATION NUMBER: US 336,672
FILING DATE: 1.1-APRL-1989
FRICK APPLICATION NUMBER: US 208,997
FILING DATE: 1.1-APRL-1989
FRICK APPLICATION NUMBER: US 208,997
FILING DATE: 1.1-APRL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 36.615
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
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Matches 1983; Conservative
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INDIVIDUAL ISOLATE:
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                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
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STREET: 350 Cambridge Avenue, Suite 250
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Patent No. 5885768
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis E Virus Per
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
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US-07-876-941A-1
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BURNA SEQUENCE, FIGURE
US-07-870-985A-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                     NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY, AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic
STRANDEDNESS:
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5627 AGTCCGCTTTTACCCCTTCAGGACGGCACCAATAACCCATATAATGGCCACGGAAGCTTCT 5686
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FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 17-JUN-1988
ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHORE: (650) 324-0880
TELEPHORE: (650) 324-0880
TELEPHORE: (650) 324-0880
TELEPHORE: (650) 324-0880
TELEPHORE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRARACTERISTICS:
LENGTH: 7195 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HEV
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HYPOTHETICAL:
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; LOCATION:
US-08-478-507-6
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No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
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                                                                                                                                                                                                                                                                 1846 TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGGCCCGCGCC
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                                                                                                                                                  1741 ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
                                                                                                                                                                                                                                     1801 TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC
                                                              CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC
                                                                                                  1726 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER BE Floppy disk
COMPUTER BE Floppy disk
COMPUTER: BM PC COMPATIBLE
COMPUTER BE FLOPPY DISK
SOFTWARE: PATENTINE Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-001-1994
FILING DATE: 25-001-1994
PRIOR APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-001-1994
PRIOR APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-001-1994
FILING DATE: 05-001-1994
FILING DATE: 05-001-1994
FILING DATE: 05-001-1994
FILING DATE: 05-001-1990
FILING DATE: 05-001-1990
FILING DATE: 05-001-1990
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk B
TITLE OF INVENTION: DNA Sequences of
TITLE OF INVENTION: No. 6120988-A/NO
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UNN-1989
PRIOR APPLICATION DATE: US 07/336,672
APPLICATION NUMBER: US 07/336,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08478507
Patent No. 6120988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reyes,
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541 AATTATGCCCAGTACCGGGTTGCCCACAATCCGTTACCGCCCGC	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGGGGACTGCCGACCGCGACTGCCGGG

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GACCAGICCACTIATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTT 1500
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                                                                                        5987 CAIGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
                                GTCGGTGAGATCGGCCGCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
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                                                                                                                                   TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA
                                                                                                                                                                                                                                                GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTTGCATA
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APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 7195 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TYPE: nucleic acid
STRANDENNESS: double
TYPE: Nucleic acid
ANATICAL: NO
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100.0%; Score 1983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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28..5106
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LOCATION:
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US-09-128-275A-6
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100.0%; Pred. No. 0;
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APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             ALIGNATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REPERENCE/DOCKET NUMBER: 4600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 7195 base pairs
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Matches 1983; Conservative
                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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5106..5474
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ORIGINAL SOURCE:
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FEATURE:
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LOCATION:
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Patent No. 6379891
GENERAL INFORMATION:
APPLICANT: Reporty R
APPLICANT: Bradley, Daniel W
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: DNA Sequences of Signed Benefits Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                           6767 CTCCGCGGTAAGCTCTTTCTGGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT
                                                                                                                                                                                          CTCCGCGGTAAGCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
FRICH APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/553,427
FILING DATE:
FRIOR APPLICATION DATA:
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC Compatible
PC PC-DOS/MS-D
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OPERATING SYSTEM:
SOFTWARE: PatentI
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	Search completed: August 21, 2004, 18:10:41 Job time : 159.606 secs
481 AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540 5627 AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT 5686 541 AATTATGCCCAGTACCGGGTTGCCCGTGCCCAATACCGCTCGCCGCTGGTCCCCAAT 5746 601 GCTGTGGGCGGTTACGCCATCTCATCTCTGGCCACGCCGCTGGTCCCCAAT 5746 601 GCTGTGGGCGGTTACGCCATCTCATCTCTGGCCACGACGCCCGCTGGTCCCCAAT 5746 601 GCTGTGGGCGGTTACGCCATCTCCATCTCTTCTGGCCACGACGCCCCCCCC	961 TCCCGITATTCCAGCACTGCTCACCACCGCCTTCGTCGCGCGCGCG
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Sequence 10, Appli
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10985.769 Million cell updates/sec
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Sequence 1,
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Sequence 4
Sequence 4
                                                                                              August 21, 2004, 15:15:13 ; Search time 886.671 Seconds
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                    3228839 seqs, 2456066551 residues
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Sequence 164, App
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Sequence 89, Appl
Sequence 89, Appl
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Sequence 9, Appli
Sequence 7, Appli
Sequence 129, Appli
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## ALIGNMENTS

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US-09-769-066-1

Sequence 1, Application US/09769066

Patent No. USZ0020107360A1

GENERAL INFORMATION:

MCAtee, C. Patrick

Yarbough, Patrice O.

Yarbough, Patrice O.

TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: USA

CUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/769,066

FILING DATE: 24-Jan-2001

CLASSIFICATION AUMBER: 08/542,634

FILING DATE: 100 AUMBER: 38/58

REGISTRATION NUMBER: 33/875

REGISTRATION NUMBER: 34-0860

TELEFORMUNICATION INFORMATION:

NAME: Fablan, Gary R.

RESERENCE, DOCKET NUMBER: 34-0860

TELEFORMUNICATION INFORMATION:

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                   GACTITGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACAATACGCGGGTC
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: Hepatitis
                                                      ORF-2
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1:-09-769-066-1
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Similarity 100.0%;
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APPLICANT: Reves, Gregory R.
Bradley, Daniel W.
Twu, Jr.-Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
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FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
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APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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SEQUENCE DESCRIPTION: SEQ ID
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LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION:
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MOLECULE TYPE: CDNA to mRNA
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                                                                                        TAG 1983
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US-10-165-868-3
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                                                         Tam. Albert W.

Krawczynski, Krzysztof Z.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCGCCCTCGGCCTATTTGTTGCTGCTCCTCATGTTTTTGCCTATGCT
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                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE, FIGURE; BURMA SEQUENCE, FIGURE; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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PILING DATE: 20-APRIL-1992

PELING DATE: 20-APRIL-1992

APPLICATION NUMBER: US 822,335

FILING DATE: 17-JAN-1992

APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

APPLICATION NUMBER: US 420,921

FILING DATE: 13-OCTOBER-1989

APPLICATION NUMBER: US 367,486

FILING DATE: 11-APRIL-1989

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

APPLICATION NUMBER: US 208,997

FILING DATE: 17-JUNE-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, GATY R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0093.30

TELECOMMUNICATION INDERER: 33
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100.0%; Pred. No. 0;
ive 0; Mismatches
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APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
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Best Local Similarity
Matches 1983; Conserv
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                                         GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                           GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC
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Publication No. US20030143241A1
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
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181 CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGGCTGGACCTCGTGTTCGCCAACCCGCC 240	3 <del>- 8</del>	1 AGACCTACCACAGCTGGGCGCGCGCTAACCGCGGTCGGTC	0-0		ITTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGCTTCT		CTGGCCACACACCACCACCCGACG 66	GGCATA 72	AGCTGGCGCTCC 78	GTTATGCTTTGCATA 84	GGCTGTTG 90	ACGCGGGTC 96.	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020 			120	(b)—(l

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                                                              Version #1.25
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REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
                                                                                                                                                   FILING DATE: *CURROWN APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UN-1989
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/316,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UN-1988
ATTONNEY/AGENT INFORMATION:
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   COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIR Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,410
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                                                                                                                                        APPLICATION NUMBER: 09/128,275
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          E: (650) 324-0880 (650) 324-0960
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TELEPHONE: (650) 324-0880
                                                                                                          FILING DATE: 07-May-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7195 base pairs
TYPE: nucleic acid
STRANDEDNESS: HEV - Burm
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SEQUENCE CHARACTERISTICS:
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28..5106
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
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Best Local Similarity 100.
Matches 1983; Conservative
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552 444 58 58 56	CTTGACGGTGGCCCCCTCCTCCACGAGTACTCGAAGACCTTCTTTGTCCTGCG 162 CTTGACGGTCGCCCCTCCACCATCAGAGTACTCGAAGACCTTCTTTGTCCTGCG 162 CTTGACGGTCGCCCCCTCCACCATCCAGAGTACTCGAAGACCTTCTTTGTCCTGCCG 576 CTTGACGGTAAGACTTCTTTGTCCTGCCG 676	1021 6767 1681 6827	QY         1741 ATTTCACTTACACCACTAGGCTGGGTGCTGGTCCGTTTCTGCGGTTGCCGTT         1800           Db         6887 ATTCCACTTACACCACTAGGCTGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT         6946           QY         1801 TTAGCCCCCCACTTGCGCTAGGATTGCTTGAGGATACCTTGGACTTGCCGCGCGCG	706( 192)	17	SEST	TITLE OF INVENTION: COMPANY, Ltd. TITLE OF INVENTION: COMPANY, Ltd. TITLE OF INVENTION: COMPRESING SAID FRAGMENTS AND THE DIAGNOSTIC KITS FILE REFERENCE: IEC010037PCT CURRENT APPLICATION NUMBER: US/10/381,770	; CURRENT FILING DATE: 2003-07-16; NUMBER OF SEQ ID NOS: 12; SOFTWARE: Patentin Version 3.1; SEQ ID NO 5; LAMETHOUS OF TABLES	F-1 Z-1	Query Match Best Local Similarity 94.4%; Score 1805.4; DB 13; Length 1990; Best Local Similarity 94.4%; Pred. No. 0; Matches 1872; Conservative 0; Mismatches 111; Indels 0; Gaps 0;	ATGITITIGCCIAIGCIGCCGCGCCA 60

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GACTITGCCCITGAGCTIGAGITICGCAACCITACCCCCGGTAACACACAATACGCGGGIC 960
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                                                                                                                 Score 1793.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.4%;
Matches 1871; Conservative (
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; NUMBER OF SEQ ID NOS:
; SOFTWARE: PatentIn veri
; SEQ ID NO 6
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: hepatitis E
US-10-381-770-6
   NOS:
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Publication No. US20040052813A1
GENERAL INFORMATION:
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Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: «URKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293,30
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 0;
tive 0; Mismatches
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CLASSIFICATION: <Unknown>
                                                                                                     Sequence 3, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
APPLICANT: Fuerty, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice (
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TELEFAX: (415) 324-0960
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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STRANDEDNESS: double
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Matches 1647; Conservative
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US-09-769-066-2		-	
Query Match 69.8%; Score 1384.6; Best Local Similarity 81.1%; Pred. No. 0; Matches 1609; Conservative 0; Mismatches	384.6; DB 9; Length 2058; fo. 0; atches 374; Indels 0; Gaps 0;	y da	1021 CTCACCACCACGGCTGCTACCGCTTTATGAAGGACCTCTATTTACTAGTACTAATGGT 1080 1021 CTGACCACACACTGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGG 1080
1 AIGCOCCTCGGCCTATTITGTIGCTGC	ATGCGCCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCCGCGCCA 60	δ a	1081 GTCGGTGAGATCGGCCGCGGGGATAGCCCTCACCCGGTTCAACCTTGCTGACACTCTGCTT 1140
61 CCGCCGGTCAGCCGTCTGGCCGCCGTC	STGGT       STGGT	λο qα	1141 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCGGCTGTTCTACTCCCGTCCC 1200
121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTGGCAATCCCCTATATTCATCAA 	CCAAC 18       CCAAC 18	& A	1201 GITGICICAGCCAAIGGCGACIGITAAGITGIAIACAICIGIAGAGAAIGCICAG 1260 
181 CCCTTGGCCCCGGATGTCACCGCTGGGGGCGGGGCTGGACCTCGTGTTCGCCAAC	GCCGGGGCTGGACTCGTGTTCGCCAACCCGCC 240	čo a	1261 CAGGATAAGGGTATTGCAATCCCGCATGACCTTGACCTCGGAGAATCTCGTGGGTTATT 1320 
241 CGACCACTCGGCTCCGCTTGGCGTGACC	CGACCACTCGGCTTGGCGTGACCAGGCCCAGGCCCGCCGTTGCCTCACGT 300	y d	1321 CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC 1380
301 AGACCTACCACAGCTGGGGCGGCGCTAACCGCGGTCGCTCCGGCCCATGACA(	CCCG	λ d	1381 CCTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT
361 CCAGTGCCTGATGTCGACTCCGGGGGGGGGGGGGGGGGG	CAGTGCCTGATGTCGACTCCCGGGGGCGCCATCTTGCGCGGGAGTATAACCTATCAACA 420 	y d	1441 GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 1500
421 TCTCCCTTACCTCTTCCGTGGCCACCG	CTCTT 48	ζζ Op	1501 GTTAATGTTGCGACCGCGCGCGGCGCTGCCCGGTCGCTCGATTGGACCAAGGTCACA 1560 
481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGA 	CTTCT   1  CCTCC	çç q	1561 CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG 1620
541 AATTAIGCCCAGTACCGGGTIGCCCGTGCCACAATCCGTTACCGCCCGCTGGTCCC	CAAT     TAAT	QV Db	1621 CTCCGCGGTAAGCTCTTTCTGGAAGGCAGGCACACTAAAGCCGGGTACCCTTATAAT 1680 
601 GCTGTCGGCGGTTACGCCATCTCCATCTC	GACG 	O.y.	1681 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT 1740
661 TCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGG		& A	1741 ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 1800 [
721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCG 	CTCC 78     CTCG 78	Qy	1801 TIAGCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC 1860
781 GTGGAGACCTCTGGGGTGGCTGAGGAGA 	CATA 84	<i>&amp;</i> 8	1861 CATACTITIGATGATITICICCCCAGAGIGCCGCCCCCTIGGCCTTCAGGGCTGCGCTTTC 1920 
841 CATGGCTCACTCGTAAATTCCTATACTAA 	STIG  -	O.Y	1921 CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGGTAAAACTCGGGGGGTTG 1980 
901 GACTTTGCCCTTGAGCTTGAGTTTCGCAR 		<i>&amp;</i> 8	1981 TAG 1983 
961 TCCGTTATTCCAGCACTGCTCGCCACCC 	TCCCGTTATTCCAGCACTGCTCGCCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020 	RESULT US-10-1	SULT 9 -10-165-868-4 Sequence 4, Application US/10165868

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                                APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374; Indels
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: ORF 2, MEXICO, FIGURE SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/07/870,985A
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20.APRIL-1992
APPLICATION NUMBER: US 622,335
FILING DATE: 17.JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 15.APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13.COTOBER-1999
APPLICATION NUMBER: US 420,921
FILING DATE: 14.JUNE-1999
FILING DATE: 16.JUNE-1999
                                                                                                                                                                                   ADDRESSE: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.0%; Score 1368.6; Best Local Similarity 81.0%; Pred. No. 0; Matches 1606; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2055 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ORIGINAL SOURCE:
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STRANDEDNESS: double
            US20030143241A1
                                                                                                                                                           NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                               COUNTRY: USA
                             GENERAL INFORMATION:
             Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-165-868-4
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0; Mismatches 374; Indels
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 337,486
FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1988
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1988
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APPLICATION DATA:
FILING DATE: 06-Jun-2002
CLASSIFICATION: vUnknown>
PRIOR APPLICATION DATA:
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Publication No. US20030143241A1
GENERAL INFORMATION:
APPLICANT: Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
FILING DATE: cUnknown>
FILING DATE: cUnknown>
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 14-UN-1989
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: PETILON NUMBER: 45,995
FELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
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TELEROMMUNICATION INFORMATION:
SEQUENA: (650) 324-0860
TELEROMMUNICATION INFORMATION:
SEQUENA: (650) 324-0860
TELEROMMUNICATION INFORMATION:
SEQUENA: (650) 324-0860
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7171 base pairs
TYPE: nucleic acid
STRANDEDNESS: Composite Mexico strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1368.6; I
Pred. No. 0;
0; Mismatches
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ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA
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Matches 1606; Conservative
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2) AGACCTACGACAGGGGCGCGCGCTAACCGCGGTCGCGTCCGGCCATGACACCGGGGTCGTCCGGGCCATGACACCCGGGGTCGGTC	0 Qy 361 3 Db 5477	0 Qy 421 3 Db 5537	O Qy 481 P	0 Qy 541 3 Db 5657	0 Qy 601 3 Db 5717	661	Qy 721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATGGTAACCAAGGCTGGCGCTCC	Qy 781 E virus cd Db 5897	the same	OY 901 GACTITGCCCTTGAGTTTGGCAACCTTACCCCGGTAACACCAATACGCGGGTCTC	Oy 961 TCCCGTTATTCCAGCACTGCTCGCCACGCCTTCGTCGCGGACGGA	Oy 1021 CTCACCACCACGGCTGCTACCGCTTTATGAAGGACCTCTATTTACTAGTACTAATGGT	1; Qy 1081 Db 6194	6 Qy 1141	Db 6254 6 Qy 1201	6 0314 GTIGT 6 07 1261 CAGGA	Db 6374	300 bb 6434 CAGGATTATGACAACCAGGATGAGGAGGAGCCCACCCGGCGGCCACCACCAGGATGAGGAGGAGGATGAGGAGGAGGCCCACCCGGCGGCCACCAGGATCTCGG
	TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCT 174 [{{{	180	9	CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC 192	CAGICIACIGICGCIGAGCITCAGCGCCTIAAGAIGAAGGIGGGIAAAACTCGGGAGIIG 1981 	1981 TAG 1983     7034 TAG 7096	RESULT 12 US-10-239-090A-49 HIS/10239090B	pati	TENTION: from Japanese, chip including the same, kit including TENTION: detecting hepatitis E virus using the same (SE: 0250741P	NG DATE: 2003-07-24 MATION NUMBER: JP2001-191837 DATE: 2001-06-25 O ID NOS: 57	Q ID NO 49 LENGTH: 7180 TYPE: DNA PROALITIS E VITUS Mexico(W74506)		0; Mismatches 374; Indels 3; Gaps ITCTTGCTGCTCCTCATGTTTTGCCTATGCTGCCGGCCA 60				CCCTTCGCCCCGATGTCACCGCTGCGGCCGGGGTGGACTTCGTGTTCGCCAACCGGC 240	3TCGT 30

61 CCGCCCGGTCAGCCGTCTGGCCGCGCGCGCGCGCGCGCGTTCCGCGCGTTCCGCGCGTTCCGCGCGCGTTCCGCGCGCGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	
2 4 2 2 4 2 4 2 4 2 4 4 4 4 4 4 4 4 4 4	6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B
1411	RESULT 13 US-10-239-090A-49 IS-20-239-090A-49 Sequence 48, Application US/10239090A Publication No. US20040101820A1 GENERAL INFORMATION GENERAL INFORMATION: TITLE OF INVERTION: Erom Japanese, chip including the same, kit including the same, TITLE OF INVERTION GENERAL TOSHIBA TITLE OF INVERTION: FILE REPERENCE: 0250741P TITLE OF INVERTION GENERAL TOSHIBA TITLE OF INVERTION GENERAL TOSHIBA TITLE OF INVERTION CONTRACT ADDAMES: US/10/239,090A TITLE OF INVERTION OFFICE TO 030-07-24 PRIOR PAPLICATION NUMBER: US/10/239,090A CURRENT FILING DATE: 2001-06-25 NUMBER OF SEQ ID NOS: 57 SEQ ID NOS 48 LENGTH: 7230 TYPE: DNA CORGANISM: Hepatitis E Virus Japan JRA1(AP003430) US-10-239-090A-48 Set Local Similarity 80.64; Score 1367.6; DB 17; Length 7230; Matches 1598; Conservative 0; Mismatches 384; Indels 0; Gaps 0; Matches 1598; Conservative 0; Mismatches 384; Indels 0; Gaps 0; Matches 1598; Conservative 0; Mismatches 2384; Indels 0; Gaps 0; Matches 1598 Argedecenterical Contrafficient Contrafficent Contrafficient Contrafficie

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                                                                                                               Japan JKK-Sap (AB074917)
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                                                                                                                                                                                     Score 1347.6;
Pred. No. 0;
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                   Query Match 68.0%;
Best Local Similarity 80.1%;
Matches 1584; Conservative
                                                                                              TYPE: DNA ORGANISM: Hepatitis E Virus
PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SEQ ID NO 47
LENGTH: 7228
                                                                                                                           , ORGANISM: Hep
US-10-239-090A-47
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Publication No. US20040101820A1
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA TOSHIBA
TITLE OF INVENTION: Polynucleotide probe and primer derived from hepatitis E virus cc
TITLE OF INVENTION: From Japanese, chip including the same,
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REFERENCE: 0250741P
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; Sequence 45, Application US/10239090A
; Publication No. US20040101820A1
; GENERAL INFORMATION:
; APPLICANT: KABUGHIKI KAISHA TOSHIBA
; TITLE OF INVENTION: Polynuclectide probe and primer derived from hepa
; TITLE OF INVENTION: From Japanese, chip including the same
; TITLE OF INVENTION: detecting hepatitis E virus using the same
; TITLE OF INVENTION: detecting hepatitis E virus using the same
; CURRENT APPLICATION NUMBER: US/10/239,090A
; PRIOR PILING DATE: 2003-07-24
; PRIOR PILING DATE: 2001-06-25
; NUMBER: QEO ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                     Length 7233;
                                                                                                                                                                                                                                                                                                                                                                                               Score 1346.8; DB 17; Lengt
Pred. No. 0;
0; Mismatches 397; Indels
                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Hepatitis E Virus Japan JMY-Haw(AB074920)
US-10-239-090A-45
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Best Local Similarity 80.0
Matches 1585; Conservative
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6967 CTAGCCCCACACTCGGCCCTCGCCGCTTAGAGACACCGTTGATTACCCCGCCCG	1861 CATACTITIGAEGATITICIGCCCAGAGIGCCGCCCCTIGGCCTICAGGCIGCGCIIIC 1920	cacacititentelititigecegaagiecegiaeceirogariigeaggrigearee 7086	1921 CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980	7087 CAGICTACTATCGCTGAGCTTCAGCGTCTTAAATGAAGGTAAAACCCGGGAGTCT 7146	1981 TA 1982	7147 TA 7148	
6967	1861	7027	1921	7087	1981	7147	
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Search completed: August 21, 2004, 22:41:57 Job time : 895.671 secs

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Unknown.
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ACCESSION
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                                                          August 21, 2004, 08:42:47; Search time 7630.72 Seconds (without alignments) 11246.543 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                        OM nucleic - nucleic search, using sw model
                                                                                                                                          IDENTITY NUC Gapop 10.0 , Gapext 1.0
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AR002161 Sequence
AR170405 Sequence
AR232466 Sequence
AR232464 Sequence
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AR207634 Sequence
BD189811 Polynucle
M74506 Hepatitis E
AR170407 Sequence
B17107 Hepatitis E
AR13981 Sequence
AR134194 Sequence
AR234194 Sequence
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AR234194 Sequence
AR244002 Hepatitis E
AR44002 Hepatitis E AR278906 Sequence D11092 Hepatitis E 173139 Sequence 1 AF12447 Hepatitis AR002160 Sequence AR23465 Sequence AR032463 Sequence AR032463 Sequence AR232463 Sequence AR232463 Sequence AR232463 Sequence AR232463 Sequence AR232463 Sequence AR207633 Sequence AR207633 Sequence AY204877 Heparitis AF185822 Heparitis X99441 Heparitis E D10330 Heparitis E D103103 Heparitis E L08816 Heparitis E M94177 Heparitis PAT 03-APR-1998 AF051830 Hepatitis X98292 Hepatitis E AF444003 Hepatitis AY230202 Hepatitis L25547 Hepatitis E L25595 Hepatitis E Hepatitis score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AF065061 linear DNA (bases 1 to 1980)
Reyes,G.R., Tam,A.W. and Yarbough,P.O. Hepattitis E virus peptides and methods Patent: US 5686239-A 2 11-NOV-1997;
Location/Qualifiers ALIGNMENTS Sequence 2 from patent US 5686239. SUMMARIES HPEGENSA HPCEGENOM AF065061 AF444003 AY230202 AF124407 AR002160 AR170404 AR232465 AR002158 AR232463 AR150915 AR150915 AF051830 AR234194 BD084498 AF444002 HPEORFS AR278906 AY204877 AF185822 AR170405 AR232466 AR150916 AR207634 HPENSSP AR170407 AR139826 AR167470 HPEGENA HEVORFS HPEUIGH BD189811 HPEHEV HPESVP E17109 HPECG HPEA 14 14 4 4 4 4 4 4 14 I73140.1 GI:3009279 DB Length 1980 1983 7138 7168 7168 7168 2049 2049 2094 7204 7204 7204 7204 7221 7221 7207 7207 7207 7207 7207 7194 2094 Unknown. Unclassified. Query Match REFERENCE AUTHORS TITLE JOURNAL FEATURES

WERSING AROUGLEL. GI:3963715  WERSING AROUGLEL. GI:3963715  SCHEWARDS  UNDAWA.  ONGANISM  WERSINGS  WERSINGS  UNDAWA.  WERSINGS  UNDAWA.  WERSINGS  UNDAWA.  WERSINGS  UNDAWA.  WERSINGS  UNDAWA.  WERSINGS  WERWAGYNEKI.X. and Yathoub.P.D.  TITLE  WERWAGYNEKI.X. And Yathoub.P.D.  TITLE  PEPATHESS  Location/Oualifiers  SOURCE  AUTHORS  Location/Oualifiers  Location/Oualifiers  SOURCE  AUTHORS  AUTHORS  AUTHORS  Location/Oualifiers  SOURCE  AUTHORS  AUTHORS  AUTHORS  Location/Oualifiers  SOURCE  AUTHORS  AUTHORS  AUTHORS  AUTHORS  AUTHORS  Location/Oualifiers  SOURCE  AUTHORS  AUTHORS	Gaps 0; GGCCA 60 GGCCA 60 GGCA 60 GGCA 60 GGCA 120 GGCA 120 GTCGC 180 GTCGC 240 GTCGC 240 GTCGC 300 GTCGC 300 GTCGC 300 GTCGC 340 GTCGC 300 GTCGC 340 GTCGC	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	11
481 AATCCGCCTCTGCCGCTGCAGGACGTACTATACTCACATTATGGCCACAGAGGCCTCC 541 AATTATGCACAGTACCGGCTACTATCCGTTACCGGCCCCTAGT 641 AATTATGCACAGTACCGGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT 641 AATTATGCACAGTACCGGCTTACCGCTACTACCGGCCCCTAGTGCCTAAT 641 CAGTTGGACGCTATATCCATTTCTTCTGCCCTCAAACACACAC	CCTCC 540 CTAAT 600 CTAAT 600 CTACA 660 CTACA 660 GCATA 720 GCTCG 780 GCTCG 780	8 6 8 6 8 6 8 6 8 6 8	1561   GACGGCCCCCCCCCCTCCCGACTGTTGAGCAATATTCCAAGACTTCTTTGTGCTCCCCCTT   1620     1621   CGTGGCAAGCCCTCCCGACTGTTGGCGACCACAAAAGCAGTTATCTTTGTGCTCCCCCTT   1620     1621   CGTGGCAAGCTCTCCTTTTGGGAGGCGGCACAACAAAAGCAGCTATCCTTATAATAT   1680     1621   CGTGGCAAGCTCTCTTTTGGGAGGCGGCGCACACAAAAGCAGCTCTTATAATATTT   1680     1621   AATACTACTGCTAGTGACCAGATTCTGATTGAAAAAGCAGCCACCCGGCCCTTT   1740     1621   AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATTCGGGCCCCTT   1740     1741   TCAACCTATACCACCAGGCTTGGGCGCGCGCGCCGCCGCGCGCG

	661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720 	721 GCATCTGAATTGGTCATCCCAAGCGCGCTTCACTACCGCAATCAAGGTTGGCGCTCG 780	781 GTTGAGACATCTGCTGAGGAGGAGCCCCTCCGGTCTTGTCATGTTATGCATA 840 841 CATGGCTCTCCAGTTACCCCTATACCCCTTATACCGGTGCCTTACTG 900 841 CATGGCTCTCCAGTTAACTCCTATACCCCTTATACCGGTGCCCTTACTG 900 841 CATGGCTCTCCAGTTAACTCCTATACCCATTATACCGGTGCCCTTACTG 900	901 GACTTTGCCTTAGAGCTTGGCAATCTCACCACCTGTAACACCAATACACGTGTG 960 	961 TCCCGTTACTCCAGCACTGCTCGTCACCCCGAGGGGGCCGACGGGACTGCGGAGCTG 1020		1081 GGTGAAGTCGGCGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGC 1140 		1201 GTCTCAGCCAATGGCGAGCCAACGGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 1260 		1321 GATTATGACAACCAGCATGAGCAGCATCGGCCCACCCCGTCGCGCCATCTCGGCCT 1380 [	TTTCTGTTCTCCGAGCAATGATGACTTTGGCTGTCCCTCACTGCAGCGGGGTATGAC	CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG [		1561 GACGGGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCTT 1620 [	1621 CGTGGCAAGCTCTCTTTTGGGAGCCGGCACAACAAAAGCAGGTTATCTTATAATTAT 1680	
qq	Qy Dp	oy Oy	Db Qy	Qy Qp	çy G	oy Ob	\$ g	QV qu	ζζ QΩ	çy da	% a	δ d	\$ B	k d	S G	8 B &	
	Qy 1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 1980 	RESULT 3 AR170405 LOCUS AR170405 DEFINITION Sequence 2 from patent US 6291641.		REFERENCE 1 (bases 1 to 2055) AUTHORS Fuerst, T.R., McAtee, C.Patrick., Yarbough, P.O. and Zhang, YF. TITLE Hepatitis E virus antigens and uses therefor JOHRNAL Patent: US 6291641-A 2 18-SEP-2001;	FEATURES Location/Qualifiers source 1. 2055 /organism="unknown" /mol_type="unassigned DNA"	Query Match Query Match Best Local Similarity 100.0%; Score 1980; DB 6; Length 2055; Best Local Similarity 100.0%; Pred. No. 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TECTGTTGTTCTCTCTTTTCTGCCTATGTTGCCCGCGCCA 60	61 CCGACCGGTCAGCCGTCTGGCCGCCGCGCGCGCGCGCGCG	121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	QY         181 CCCTTTGCCCCAGACGTTGCCGCTGCGGCTCTGGACCTCGCCTTCGCCAACCAGCC 240           Db         181 CCCTTTGCCCCAGACGTTGCCGCTGGGATCTGGACCTCGCCTTCGCCAACCAGCC 240	CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTGCCTCCCGTCGC	CGACCTGCCACAGCCGGGGGCTGCGCTGACGGCTGTGGCGCTGCCCATGACACCTCACACGCCTGCCCATGACACCTCACACGCCTGCCACATGACACCTGCCAACCCATGACGCCTGCCCATGACACCTCACACGACGACGCTGCCATGACGCCTGCCATGACGCCTGCCATGACACCTCACACCTGCCCATGACACCTCACACCATGACGCCTGCCATGACACCTCA	Oy 361 CCCGTCCCGGACGTTCATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT 420  Db 361 CCCGTCCCGGACGTTCATTCTCGCGGTGCAATTCTACGCCGCCAGTATATTTGTCTACT 420	Qy 421 TCACCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTT 480  Db 421 TCACCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTT 480	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 481 AATCCGCCTCTGCCGTTGCAGGACGGTACTAATACTCACATTATGGCACAAGAGGCCTCC	541 AATTATGCACAGTACCGGGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT	. Oy 601 GCAGIIGGAGGCIAIGCIAIACCATIICIIICIGGCCICAAACAACCACAACCCIACA 660

481 TCACCCCTGACATCCTCTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCCTT 480 481 AATCCGCCTCTGCAGGACGGTACTAATTTAGTCCTGTATGCAGCCCCCCTT 480 481 AATCCGCCTCTGCAGGACGGTACTAATTTAGTCCTATTGGCCACAGAGGCCTCC 540 481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATTTATGGCCACAGAGGCCTCC 540 541 AATTATGCACAGTACCGGCTTGCCTAATTATTAGTCACATAATGGCCACAGAGGCCTCC 540 541 AATTATGCACAGTACCGGGTTGCCGGCCTACTACCGGCCCCTAGTGCCTAAT 600 601 GCAGTTGGAAGTACCGGGTTGCCGCGCTACTATCGGTTACCGGCCCCTAGTGCCTAAT 600 601 GCAGTTGGAAGTTACCATTACTTTCTTTCTGGCCTCAAACCACCCCTACA 660 601 GCAGTTGGAAGCTATACCATTTCTTTCTTGGCCTCAAACAACCAAC	ANTIGGTCATCCCAAGCGACGCCTTCACTACCGCAATCAAGGTTGGCGCTCG	1021   ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA   1080     1021   ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA   1080     1021   ACCACAACTGCAGCCACCAGGTTCATGAAACTTTACCGGCCTTTAATGGGGTA   1080     1081   GGTGAAGTCGGCGGGGAAACTTCATAACTTTACCTGGACACCGCTCCTCGGC   1140     1141   GGGCTCCCGACAGAATTAATTTCGTCGGCTAACTTTAATTCCTGGACACCGCTCTCGGC   1200     1141   GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGCACTGTTTTAATTCCCGCCCG
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Db 1681 AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT 1740  Qy 1741 TCAACCTATACCACGGCTTGGGGCCGTCCGGTCGGCCGCGTTTTTG 1800  1741 TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCCGG	RESULT 4   RA232466	Description   100.0%;   Score 1980;   DB 6;   Length 2055;   Best Local Similarity   100.0%;   Pred. No. 0;   Mismatches   0;   Indels   0;   Gaps   0;   Matches 1980;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;   ATGCGCCTAGGCCTCTTTTGCTGTTGTTCTCTTTTTTGCCTAGGTGCGCGCGC

	1 CCGTCCGGACGTTGATTCTCGCGGGCGCGCGCGCGGTGTTGTTCTGCTGCGCGCGCGGTGTATTTTTTCTGCTGCGCGCCGGTGTTGTTTTTTTT	26 AATCCGCCTCTGCCGCTGCAGGACGTACTAATACTCACATTATGGCCACAGAGGCCTCC 58 41 AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCGGTCACCGCCCCTAGTGCCTAC		841 CATGGCTCTCCAGTTAACTCCTATACCATACCGGTGCCCTTGGCTTACCGGTGCCCTTAGCTGG 900	1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080
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Reyes(R., Yarbough, P.O., Bradley, D.W., and Fry, K.B.
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	Db   6557   CAGTICALTHICAGGGTCGARACTCGGGTTATATATCTCGGGCGCGCGTGGTGTGTGTGTG	RESULT 8 AR207634 LOCUS AR207634 DEFINITION Sequence 10 from patent US 6379891.

1381 TITTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGAC 6497 TITTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGAC 1441 CAGTCCACTTACGGGTCGTCAACTGGCCGGTTTATATCTCGGACACGCGTGACTTTGGTG 1501 AATGTTGCGACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG 1501 AATGTTGCGACTGGCCGGGTCGACCCGATTGTTATATCTCGGACAGCGTGACTTTGGTG 1501 AATGTTGCGACTGGCCGGGCGGTGACCCGATGACTGGTCCCCTC 1501 AATGTTGCGACTGGCGCGGGCGGTGACCCCTC 1501 AATGTTGCGACTGGCCGGAGCCGGACCCGATGGTCAAAGTCACCCTC 1601 AATGTTGCGACTGGCGCGGGCGGTGACCCCTC 1701 AATGTTGCGACTGGCCGGAGCCCGATCGCTTGACTGGTCCCAAAGTCACCCTC 1701 AATGTTGCGACTGGCGCGAGCCCGATCGCTTGACTGGTCCCAAAGTCACCCTC	0   0   0   0   0   0   0   0   0   0	QY         1741 TCAACCTATACCACCAGGCTCGGGTCGCCATTTCTGCGGCCGGTTTTG 1800           Db         6857 TCAACCTATACCACGGCTGGCTCGGTCGCCGTTTCTGCGGCCGGGTTTTG 6916           QY         1801 GCTCCACGCTCCGCCTGCTGGAGGAGATACTTTTGATTATCCGGGGCGGCGCACC 1860           Db         6917 GCTCCACGCTCCGCCTGGTGGAGGATACTTTTGATTATCCGGGGCGGCGCC 1860           CQY         1861 ACATTTGATGACTTCGGCGGAGGAGATATTCGGGGGGGGCGC 6976           QY         1861 ACATTTGATGACTTCTGCCTGAATGCCGCGCTCTAGGCTTCAGGGTTGTTTTCAG 1920           Db         6977 ACATTTGATGACTTCTGCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTTTCCAG 1920           Db         6977 ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAAGGCCTCCAGGGTTGTTCCAG 7036	QY       1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGGTAAAACTCGGGAGTTGTAG 1980         Db       7037 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTAAAACTCGGGAGTTGTAG 7096         RESULT 10       HPENSP         LOCUS       HPENSSP         LOCUS       7180 bp 88-RNA         LOCUS       HPENSSP         LOCUS       PREFINITION HEPALILIS E VIRUS (mexican strain) structural proteins and a strain of the strain of the structural proteins and a strain of the strain of the structural proteins and a structural protein a structural protein and a structural protein a structural protei	nonstructural polyprotein genes, complete cds. M74506 M74506 M74506 M74506 M74506 M74506 M74506 M74506 M74506 M74507 M74507 M74507 Hepatitis E virus Hepatitis E virus Viruses; ssRNA positive-strand viruses, no DNA stage; E-like viruses. 1 (bases 1 to 7180) Huang(.C., Nguyen, D., Fernandez, J., Yun, K.Y., Fry, K.E.	TITLE Molecular cloning and sequencing of the Mexico isolate of hepatitis by virus (HEV)  JOURNAL Virology 191 (2), 550-558 (1992)  WEDLINE 93079857  PUBMED 1448913  COMMENT Original Source text: Hepatitis E virus cDNA to genomic RNA.  FEATURES 10-0ation/Qualifiers virus"  // Mol. type="genomic RNA" // Mol. type="gen
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GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG
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5417 CGACCTGCCACAGCCGGGGCTGCGGGGCTGACGCTGTGGCGCCTGCCCATGACACCTCA
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GLESRVVFPPGNAFTAPPSEVTAFCSALYRHNRQSQRQSVIGSLMLHPEGLLGLFPPF
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PP 7 TAKEDA NACKAZU, RI TENSEI, MIYAMURA TATSUO
PC C12N15/09.CO7K14/08.C12N5/10.C12P21/02;
CC strandedenses: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source /organism='Hepatitis E virus' FT CDS

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PT /product='Structural protein'.
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GGAAAVPAVVSGYTGLILSPSQSPIFIQPTPSPPMSPLRPGLDLVFANPPDHSAPLGV
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ASHSDVRDSLARFIPAIGPVQVTTCELYELVEAMVEKGQDGSAVLELDLCSRDVSRIT
FFQKDCNKFTTGETIAHGKVGQGISAMSKTFCALFGPWFRAIEKAILALLPQGVFYGD
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IVLCSEYRQSPGAAVLIAGCGLKLKVDFRPIGLYAGVVVAPGLGALPDVVRFAGRLTE
KNWGPGPERAEQLRLAVSDFLRKLTNVAQMCVDVVSRVYGVSPGLVHNLIGMLQAVAD
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Characterization of a prototype strain of hepatitis E virus
Proc. Natl. Acad. Sci. U.S.A. 89 (2), 559-563 (1992)
92115700
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Hepatitis E virus
Viruses; ssRMA positive-strand viruses, no DNA stage; Hepatitis
E-like viruses.
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Aav54729 Aaa99259 Baf83495 Aal50386 Add24374 Abl60054 Adb97809

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Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
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89US-00336672.
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                    A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen, and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence encodes the protein from the open reading frame, ORP2, from HEV Mexico strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
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hepatitis E virus peptide
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Best Local Similarity 100.0%;

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TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAAGGTGGGTAAAACTCGGGGAGTTGTAG
                         TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGGAGTTGTAG
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a vaccine against HEV
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New viral proteins from non A-non-B hepatitis agent - used to prevent enterically-transmitted non-A non-B hepatitis virus.
                                                  Composite sequence from Mexican isolate of ET-NANB virus
                                                                          non-A, non-B hepatitis virus;
deposit number 67717; Mexico;
                                                                                                                                                                                                                                                                                                         Bradley DW, Krawxzynsk KZ,
                                                                                                                                                                                                                                                     (GENE-) GENELABS INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
(USSH ) US DEPT OF HEALTH.
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                                                                           enterically transmitted
E.coli strain BB4; ATCC
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                                                                                                                             hepatitis virus.
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27-AUG-2003
25-MAR-2003
16-JAN-1992
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The sequence from a Mexican strain of ET-NAMB virus is about 75 per cent identical to the ET1.1 sequence (see AAQ14410). The Mexican sequence was identified in a cDNA library made directly from a semi-purified human stool specimen collected from an outbreak of ET-NAMB in Telixtac.

Screening was with a serum considered to have high titer anti-ET-NAMB antibodies. Two clones were identified from a total of 60,000 screened. The sequence of these clones was subsequently localised to the 3' half of the viral genome by homology comparison to the Burma strain sequence (see AAQ14412). (Updated on 25-MAR-2003 to correct PA fiteld.) (Updated on 25-MAR-2003 to correct OS
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Matches 1980; Conservative 0; Mismatches
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QY	AAV66322  ID AAV66322 standard; CDNA; 7171 BP.  XX  XX  XX  AAV65322  XX  XX  AAV65322;  XX  XX  XX  AAV62203 (revised)  DT 25-AMG-2003 (first entry)  DT 25-AMG-2003 (first entry)  DT 25-AMG-2003 (first entry)  ET-NANB (HEV) composite Mexico strain cDNA sequence.  XX  XX  XX  Non-A.  OS non-B hepatitis E virus, HEV; Burma HEV isolate; vaccine; mexico strain; XX  XX  XX  NOn-A.  OS non-B hepatitis virus.  XX  XX  XX  YX  XX  YX  YX  YX  YX  Y
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                                                                                                                                   The present sequence represents the composite Mexico strain sequence of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF1 sequence from Burma HEV isolate (AAV66321). The protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
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                             CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGGCTGCCTCCCGTCGC
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ACATITIGATIGACTICTIGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTTCCAG
                                                                                                     ACATTIGATGACTICTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTTCCAG
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                                                                                                                                     AAV54730 standard; cDNA; 7171
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00505888.
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Best Local Similarity 100.
Matches 1980; Conservative
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11-APR-1989;
19-JUN-1989;
13-OCT-1989;
05-APR-1990;
05-APR-1991;
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30-OCT-1998
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Identifying recombinant antigen immunoreactive with antibody induced hepatitis E virus (HEV), for detecting HEV infection, comprises immunoreacting a polypeptide from an HEV genome with an HEV-positive
                                                                                                                                                                                                                                                     Claim 5; Col 69-76; 46pp; English.
                                                                                                                  GENELABS TECHNOLOGIES INC. US GOVERNMENT.
                            89US-00208997.
89US-0033672.
89US-00367486.
89US-00420921.
90US-00505888.
                                                                                   91US-00681078.
         95US-00478507
                                                                                                                                                     Krawczynski
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                                                                        05-APR-1990;
05-APR-1991;
25-JUL-1994;
                                         11-APR-1989;
16-JUN-1989;
13-OCT-1989;
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                                            GATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAG
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The present invention describes a method for identifying a recombinant antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody. The method comprises producing a polypeptide desived from an HEV genome, immunoreacting the polypeptide with an HEV-positive antiserum and selecting the polypeptide as a recombinant antigen if the polypeptide reacts with the HEV-positive antiserum. The method is useful for identifying recombinant antigen immunoreactive with antibody induced by HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also known as HEV))-specific fragments are useful for identifying ET-NANB. Or detecting ET-NANB viral genomic material in a patient sample, for the synthesis of polypeptides for use in immunoassays, and for identifying synthesis of polypeptides for use in immunoassays, and for identifying similar antigens are especially useful in the preparation of vaccine against ET-NANB inters particles for use directly as antiviral antibodies to BT-NANB virus particles for use directly as antiviral antibodies to BT-NANB virus particles for use directly as antiviral antibodies to BT-NANB virus particles for use directly as antiviral prophylaxis. The present sequence represente a specifically claimed HEV composite Mexican strain gene sequence for use in the present invention 5416 5176 5236 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGCGCCCCTCCGCTGCCTCCCGTCGC ceaccacingaciccacinadedaaancaadeceaageceeeroceeracereeerocen Arececcineeccircirriscientiericircircirciricieccinatericeccecece CCGACCGGTCACCGCCCTCTGGCCCCCCTCGTGGCGCGCCGCAGCGGCGGTACCGGCGGTGGT CCCTTTGCCCCAGACGTTGCCGCTGCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCC CCGACCGGTCAGCCGTCTGGCCGCCGTCGTGGGCGCCGCCGCGGCGGTACCGGCGGTGGT CCCTTTGCCCCAGACGTTGCCGCTGCGTCTGGACCTCGCCTTCGCCAACCAGCC Gaps Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other; ; 0 DB 3; Length 7171; 0; Indels 0, Mismatches 100.0%; Score 1980; 100.0%; Pred. No. 0; Query Match Best Local Similarity 100. Matches 1980; Conservative 5177 5237 181 5297 5357 241 121 Dp g g g  $\delta$ ò à

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Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein; immunological; diagnosis; hepatitis; infection; identification; detection; immunoreactive; hepatotropic; antiinflammatory; virucide; vaccine; antiviral; antigenic; antibody; antigen; ds.

Hepatitis E virus

JS6120988-A 19-SEP-2000.

Hepatitis E virus Mexican strain nucleotide sequence SEQ ID NO:10.

(first entry)

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Qy         1441 CAGTCCACTTACGGTCGTCAACTGGCCGGTTTATATCTCGGACAGCGTGACTTTGGTG         1500           bb         6557 CAGTCCACTTACGGGCCGTGACTGGTTGATTGTCTCGGACAGCGTGACTTTGGTG         616           carrectaractactactactactactactactactactactactacta	RESULT 7  AAF83496 Standard; CDNA; 7171 BP.  XX  AC AAF83496; XX  XX  AAF83496; XX  DE
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                                                                                                                                                                      The invention relates to an isolated DNA comprising the genome of an enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also preferred as HBV). The DNA sequences or their fragments are useful in preparing ET-NANB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The present sequence represents a Mexican strain composite ET-NANB viral
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Best Local Similarity 100.0%;
Matches 1980; Conservative 0
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GCATCTGAATTGGTCATCCCAAGCGACCTTCACTACCGCAATCAAGGTTGGCGCTCG

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The invention comprises a method for detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a sample and isolating HEV agents or nucleic acid fragments produced by the agent. The method utilises PCR - using bile from a human or cynomolgus monkey actively infected with HEV as a source of the agent. The method of the invention is used for detecting the presence of a viral agent in a sample of cultured cells infected with the agent and isolating enterically transmitted nonA/nonB HEV agents or nucleic acid fragments produced by the agent. The present DNA sequence was isolated from a Mexican strain of the Hepatitis E virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEV; enterically transmitted nonA/nonB hepatitis viral agent; Mexican strain; bile; ds.
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90US-00505888.
91US-00681078.
95US-00478507.
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The invention relates to a protein derived from an enterically transmitted non-A/non-B viral hepatitis agent. The viral proteins are useful for detecting infection by the enterically transmitted non-A/non-B (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for producing vaccines for immunising an individual against HEV hepatitis viral agent. The DNA fragments are useful for identifying and sequencing the entire viral agent and for assaying the viral agent in an infected sample. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                             New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis viral agent.
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                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 10; 81pp; English.
                                                        88US-00208997.
89US-00336672.
89US-00420921.
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91US-00681078.
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
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05-APR-1991;
25-JUL-1994;
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                                  Hepatitis E virus; vaccine; neutralising antibodies; infection; open reading frame; antibodies; ss.
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                                                                                                                                                                                                                                                                                                                                                                                  Tam AW,
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Pred. No. 0;
0; Mismatches
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                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 7; 43pp; English.
           and ORF3
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/*tag= a
/note= "ORF2"
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P-PSDB; AAR39307, AAR39308.
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Matches 1979; Conservative
           ORF2
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          strain HEV
                                                                           virus
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20-APR-1992;
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GITGAGACATCTGGTGGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATA 840
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reagents for determining HEV infection and in vaccines
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Pred. No. 0;
0; Mismatches
                          Disclosure, Page 71-72; 125pp; English.
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Similarity 99.5%;
74; Conservative
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Best Local Simi
Matches 1974;
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                                                CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
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                            CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
                                                                            AATGTTGCGACTGGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCTTC
                                                                                                                                                                             CGTGGCAAGCTCTCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT
                                                                                                                               GACGGGCGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCTT
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95US-00542634
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13-OCT-1995;
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06-AUG-1996
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                                         1918 CAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGGGTAAAACTCGGGAGTTG
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                                                                                                                                                                                                                                                                                                                                                             HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid; ds.
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and in vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus; Mexico strain.
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Matches 1638; Conserv
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Mon Aug 23 09:48:21 2004

Pred. No.

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Best Local Similarity 81.3
Matches 1612; Conservative
Similarity
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                                                                                                                                                                                                                          /transl except= pos:3739. .3741, aa:Glu
/note= "IO bp nucleic acid sequence TGGTNTTYGA has to be
inserted between nucleotides 4390. .4391 for numbering to
                                                                                                                                                                                                                                                                                                 /label= ORF-3 (AAR91815)
/label= ORF-3 (AAR91815)
/notes= "lo bp nucleot acid sequence TGGINTTYGA has to be inserted between nucleotides 4390. .4391 for numbering to conform to that given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                 /notes "10 by nucleic acid sequence TGCTNTTYGA has to be inserted between nucleotides 4390. .4391 for numbering to conform to that given in the specification"
                                                                                                       Hepatitis E virus, HEV, SAR-55 strain, enteric transmission, structural region; antigen, detection, antibody, vaccine; immunisation; infection, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated and purified hepatitis E virus strain SAR-55 DNA - encoó antigenic protein useful in diagnosis, prophylaxis and treatment hepatitis E virus infection.
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                                                                                   Hepatitis E virus strain SAR-55 cDNA (ATCC 75302)
                                                                                                                                                                                                        /*tag= a
/label= ORF-1 (AAR91813)
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                                                                                                                                                                                Location/Qualifiers
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             AAT27394 standard;
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Query Match

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Search completed: August 21, 2004, 11:00:19 Job time: 772.421 secs

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BX381961 BX381961 AL574009 AL574009 AL054280 Drosophil BX421125 BX421125 BQ144422 NF085H1D BX356664 BX356664

Drosophil

BX425797 BX425797 BX381961 BX381961

BX415926 BX464554
AL538546 AL538546
BX49688 BX349688
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BX315523 BX315523
AL550172 AL550172
AL106004 Drosophil
B195665 HVSMBn000
AL09882 Drosophil
AL201298 Tetraodon
AL060161 Drosophil
AL525224 AL525224

AL066051 Drosophil BX407485 BX407485 B1953455 HV8MEM001 BZ050854 jnr64£08 BX391246 BX391246

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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL053013. GI:4934461
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitlly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ososgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopteraygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                       BX407485
BI953455
BZ050854
BX391246
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AG060386
CNS016HG
AG043473
BX340485
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BQ144482
BX356664
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BX464554
AL538546
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CNS015WQ
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BX360624 BX360624
AL056652 Drosophil
BX403654 BX403654
                                                  August 21, 2004, 10:14:02 ; Search time 5109.13 Seconds (without alignments) 11572.836 Million cell updates/sec
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Direct Submission

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

Bp 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BAGs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutcyo Oscegawa and

Aaron Mammoser: in Pieter de Jongs a laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

sogenic strain y2, cn bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS0052P BACKLIP16 of RPCI-98 library from Drosophila melanogaster genome survey sequence TET3 end of BAC # BACKLIP16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 CACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTGCCTCCCGTCGCCGAC 304
                                                                                                                                    /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSFORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebrydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                    3.1%; Score 61.8; DB 13; Length 1201; llarity 10.0%; Pred. No. 0.00088; Conservative 160; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 CTGCCACAGCCGGGGCTGCGGCGCTGACGGC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 SSSSASSSSSSSSSSTSKWSSTASSSSS 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
                              organism="Homo sapiens"
                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI072YL05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fly), genomic survey sequence. AL056652
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Best Local 8
           source
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CNS0052P/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 bp mRNA linear EST 05-MAY-2000:
BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1072YL05 3-PRIME, mRNA sequence.
BX360624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 TACCGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           802
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPR Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 WSAGGGGGGTGSTSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSGSSSSSTSBBSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TCATCCAACCACCCTTTGCCCCAGACGTTGCCGCTGCGTCCGGGTCTGGAACCTCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 TCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGGCCCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 TGCCTCCCGTCGCCGACCTGCCACAGCCGGGGCTGCGCGCTGACGGCTGTGGCGCCTGC
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BP 191 91006 EVRY cedex - France
BP 191 1006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.r
Contact : Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO72CF03NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 925;
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                                                                                                                                                                                                                                                                                melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 148; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.2%; Score 62.4; DB 294.6%; Pred. No. 0.00056;
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                                                                                                                                                                                                                                                                           /organism="Drosophila mel.
/mol_type="genomic DNA"
/db_xref="teaxon:7227"
/clone="BACR19D16"
/clone lib="RPCT-98"
/note="end : TET3"
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Homo sapiens
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                                                                                                                                                                                                                                                       1. 925
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                               found at
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VS 924
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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission Submission Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr. - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                        145 CAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCTTTGCCCCAGACGTTGCCGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                              205 GCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGCGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 GATCAGGCCCAGCGCCCCTCCGCTGCCTCCCGACCTGCCACAGCCGGGGCTGCG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSO16KT 1013 bp DNA linear GSS 26-JUL-15
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                      85 CGTCGTGGGCGCGCGCGGCGGTACCGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCT
                                                                                                                                                                                            25 ITGTICCTCTTGTTTCTGCCTATGTTGCCCGCCCACCGACCGGTCAGCCGTCTGGCCGC
                                                                                                                                                           Gaps
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                       ;
0
                                                                                                              Length 1103;
                                                                                                            3.0%; Score 59.4; DB 13; Length 28.0%; Pred. No. 0.0033; tive 93; Mismatches 151; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN16J16"
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 CCCCCCCTYYYTCCSCCCMCCCCCCMYYYMMMC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCTGACGCCTGTGCCCATGACACCTCACCC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey sequence.
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                                                                                                                                                     95; Conservative
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                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequencoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fullength.hnvitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FP1.
                                                                                                                                                                                                                                                                                                                                    676 TCWTHTNSNTYTMVTYVTTTHHTYTNTCCYYCCCCCCYYCSCCBYBCNTSCSYYSYSBCS 617
                                                                                                                                                                                                                                                                                                                                                                           GCCGTCGTGGGCGCCGCAGCGGCGGTACCGGCGGTTTCTGGGGTGACCGGGTTGATT 142
                                                                                                                                                                                                                                                                                                                                                                                                     GCSSSSSSCSGSSBYSCCCBCCCBGYCGCYSBVCSSBSSTBSSVSGSBSSTSGTGCK 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCTTTGCCCCAGACGTTGCCG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIGCGICCGGGICTGGACCTCGCCTTCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #96 GKSGGKSSGKGGGBKSGGKGYCYCETYCCSBSSBCCSSSSSSTSKCCSGGSSSTKCGSSS 437
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched,
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                               Length 844;
                                                                                                                                                                                                         ch 3.0%; Score 60.2; DB 29; Length Similarity 19.4%; Pred. No. 0.0018; 59; Conservative 131; Mismatches 114; Indels
                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xeef="taxon:7227"
/db_xeef="ARCR11P16"
/clone="lab="RRCI-98"
/note="end: TET3"
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Lii,W.B. Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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Location/Qualifiers
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BX403654.1 GI:30762430
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                       GITGAITCTCAGCCCTTCGCAAICCCCTATATTCAICCAACCAACCCTTTGCCCCAGAC 195
                                                                                                                                                                                                                                                                                                                                       GITGCCGCTGCGTCCGGGTCTGGACCTTCGCCAACCAGCCCGGCCACTTGGCTCC 255
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                                                                                                                                             CITITIGCTGTTGCTCCTCTTGTTTCTGCCTATGTTGCCCGCCCCCCCGACCGGTCAGCCG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
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                                                           Length 1000;
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                                                             DB 13;
                                                             57.6; DB 1
No. 0.0085;
Library was not normalized."
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/organism="Drosophila
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Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
BR 191 91006 ENRY cedex - France
EMail: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed belongs to sequence cluster 6789.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AS005ZDD2QP1&cluster=6789.f. Contact :
Feng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0AS005ZD02QP1.
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/clone_lib="Homo sapiens PLACENTA"
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/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
double-strand clipo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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                                                                                                                                                                                                                                                                                                                                               ACGITGCCGCTGCGGGTCTGGACCTCGCCTTCGCCAACCAGCCCGGCCACTTGGCT 253
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1. (bases 1 to 1000)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                          73
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                                                                                        cechshhynechhonersheneckecshroveceesschneckeensdybebedeere
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      Length 1013;
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    tch 2.9%; Score 58.2; DB 29; Length al Similarity 26.7%; Pred. No. 0.0061; 108; Conservative 114; Mismatches 182; Indels
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BX407619/c
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231 861 801

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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
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                                                                                                                                                                                                                                                                                                      378 SSCCSBSSSSBBCCKGGSKCCCCBTKCCCKCCCKSCCCBKBCCCBBBCCCSBKCCC 919
                                                                                                                                                                                                                                                                              112 GGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCAT 171
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB030ZE01FP1&cluster=8556.f. Contact
cgi-bin/cluster.cgi?seq=CLOBB030ZE01FP1&cluster=8556.f. Contact
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB030ZE01FP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            1038 CCSSKCCCCCCKNSKCSKCCCCCSSSGGCCCCCCCKBCGCCBCCCCCCSSCCCCCSC
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8556.f
more information about this cluster, see
                                                                                                                                                       5.
                                                                                                           Length 1203;
                                                                                                                                                   55; Mismatches 138; Indels
                                                                                                             DB 29;
                                                                                                         Score 57.2; DB : Pred. No. 0.012;
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                                                                                                           2.9%;
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at GEPH (Centre d'Etde du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS015Y4 1203 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                           Length 1101;
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/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E10"
                                       2.9%; Score 57.4; DB 29;
16.6%; Pred. No. 0.01;
                                                                                 Conservative 195; Mismatches 165;
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For

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AL574009 1201 bp mRNA linear EST 31-MAY-2003 AL574009 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI053YA04 3-PRIME, mRNA sequence.
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                                                                                                                                431 KNYNYKKKKKKKKKKNNNNNNCNANNYMANNKNKKKKNNKNNNNTKNNMNNNCNKMNNKONKKONN 490
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                                                                   CNCNCMAAKCCNNACKANNNKKKMKACNANNNNKCKMMNNKKKKKKKKCMNKNKKKKKMMNK
                                                                                                     184 ITTGCCCCAGACGTTGCCGCTGCGTCCTGGACCTCGCCTTCGCCAACCAGCCCGG
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                                CGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTTCTGCCTATGTTGCCCGCGCCCACCG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Mismatches 489; Indels
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Conservative 270;
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BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI072YF05 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Full-length CDNA libraries and normalization
Nupublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO72CCG3NP1.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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   pCMVSPORT 6 vector
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                                                                          Length
                                                                                                          Indels
                                                                      2.9%; Score 56.6; DB 13;
llarity 30.0%; Pred. No. 0.014;
Conservative 79; Mismatches 140;
   the Not I and EcoRV sites of the Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YF05"
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                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.ons.fr, Wew.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10873.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bhi/Cluster.cgi?seq=CS0D1053BA02N1kcluster=10873.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: Gilang@lifetech.com URL:
Feng Liang Email: Liang@lifetech.com URL:
Feng Liang Email: Liang@lifetech.com URL:
Lication/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTCTGGACCTCGCCTTCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGCGAGATCAG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 GCCCAGCGCCCCTCCGCTGCCTCGCCGACCTGCCACAGCCGGGGCTGCGGCGCTG 330
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="Ist strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                     Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12933798.
Contact: Genoscope
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  Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1053YA04"
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Matches 94;
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BP 191 91006 EVRY cedex - France
Bmail: sequenéscepe.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3904.f For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 2.7%; Score 53.8; DB 29; Length 1 Similarity 18.6%; Pred. No. 0.067; 64; Conservative 137; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BACR10E16"
/clone_lib="RPCI-98"
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BX35664 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO15YB03 3-PRIME, mRNA sequence.

BX356664
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: sequefe@qenoscope.cns.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulliength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO15CA02NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."
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The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert Length: 993 Std Brror: 0.00 Plate: 085 row: H column: 11
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48.7%; Pred. No. 0.1;
tive 0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF085H11DT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
                                                                                                                                                                                                             Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
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Homo sapiens
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/clone="CSD00010M04"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
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NF085H11DT1F1095 Drought Medicago truncatula cDNA clone NF085H11DT
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                                                     http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG001BG02NP1&cluster=3904.f. Contact
cgi-bin/cluster.cgi?seq=CSODG001BG02NP1&cluster=3904.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG001BG02NP1.
Location/Qualifiers
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                            more information about this cluster, see
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/tissue type="thAcknya"

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V

sites of the pCMVSPORT 6 vector. Library was normalized."
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organism="Homo sapiens"
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/cgn2 6/ptodata/2/ina/PCTUS COMB.seg:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ORF-2 region
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NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.35, G32P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGHH: 1980 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILLING DATE: 09-MAY-1994
CLASSIFICATION: 435
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US-07-876-941A-1
US-09-128-275A-6
US-09-553-427-6
US-09-553-427-6
US-08-259-148A-10
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US-07-870-985A-10
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100.0%; Pred. No. 0;
iive 0; Mismatches
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Patent No. 5686239
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1980; Conservative
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STRANDEDNESS:
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ZIP: 94063
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STREET: 50
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STATE: CA
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	APPLICANT: Reyes, Gregory R.  APPLICANT: Bradley, Daniel W.  APPLICANT: Twu, Jr-Shin  APPLICANT: Tam, Albert W.  APPLICANT: Krawczynski, Krzysztof Z.  APPLICANT: Yarbough, Patrice D.  TILLE OF INVENTION: Hepatitis E Virus Vaccine and Method
1 MTGGGCCTMAGGCCTTTTTGCTGTTTGTTTCTTTTTTTTTGCCTMTGTTTGCCGGGGGGGG	

us-09-851-410a-10\_copy\_5117\_7096.rni

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                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/259,148A
FILING DATE: 13-7UN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                 3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
AP
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILLING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38,615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2055 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 1980; Conservative
NUMBER OF SEQUENCES: 60
                                                                                                                                                                  ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
US-08-259-148A-4
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MOLECULE TYPE:
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                                                 ADDRESSEE:
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                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 4600-0093.38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPA: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 11-AUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: SHOLTZ. CHAILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
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Best Local Similarity 100.
Matches 1980; Conservative
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                                                                                          1381 TITICIGITCICCGAGCAAAIGAAGTACTITGGCIGTCCCTCACTGCAGCCGAGTAIGAC
          GATTATGACAACCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCT
                                                GATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.-Shin
APPLICANT: Twu, Jr.-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/484,054
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
CAA
COUNTRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Palace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08484054 Patent No. 5770689
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US-08-484-054-4
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b 661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720 y 721 GCATCTGAATTGGTCATCCAGGGGCGCTTCACTACCGCAATCAAGGTTGGCGCTCG 780	y 781 GTTGAGACATCTGGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATA 840	y 841 CAIGGCICTCCAGTIAACTCCTAIACCAAIACCCCTTAIACGGGGGCCCTTGGCTIACTG 900	y 901 GACTITGCCITAGAGCITGAGTITCGCAATCICACCACCACCAAIACACGGGGG 960	y 961 TCCGGTDACTCCAGCACTGCTCGTCACTCCGCCGAGGGGCCGACGGGACTGCGGAGCTG 1020	y 1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080	1081 GGTGAAGTCGGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGC	1141 GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCG	1201 GTCTCAGCCAATGGCGAGCCAACGTGAAGCTCTATACATGAGTGGAGAATGGTCAGCAG [	1261 GATAAGGGTGTTGCTATCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAG 1261 GATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAG 1261 GATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGTCATTCAG	1321 GATTATGACAACCAGGATGAGGACCCCCCCCCGTCGCCTGCGCCTTCGGCCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCTCGGCCTTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCTCGGCCTTCGGCCTTCTCGGCCTTCGGCCCTTCTCGGCCTTCTCGGCCCTTCTCGGCCTTCTCGGCCCTTCGGCCTTCTCGGCCTTCTCGGCCCTTCTCGGCCTTCGGCCTTCGGCCCTTCTCGGCCCTTCTCGGCCCTTCGGCCTTCGGCCCTTCGGCCCTTCTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCTTCGGCCTTCGGCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCTTCGGCCCTTCGGCCCTTCGGCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCCCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGGCCTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCTTCGGCTTCGGCCTTCGGCTTCGGCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGCCTTCGGCCTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGGCCTTCGGCCTTCGGCCTTCGGCCCTTCGGCCTTCGGCCTTCGGCCCTTCGGCCTTCGCCCTTCGGCCCTTCGCCTTCGCCCCTTCCTTCTT	1381 TITICICITCICCAGCAAATGATGTACTITGGCTGTCCCTCACTGCAGCCCAACTATGAC 1381 TITICIGITCTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGAC	1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTTGGTG 1	y 1501 AATGTTGCGACTGGGCGCGGGCCGATCGCTTGACTGGTCCAAAGTCACCCTC 1560	1561 GACGGGCGCCCTCCCGACTGTTCAGCAATATTCCAAGACATTCTTGTGCTCCCCTT	1621 CGTGGCAAGCTCTCTTTTGGGAGGCCGCACAAAAGCAGGTTATCCTTATAATTAT 1621 CGTGGCAAGCTCCTTTTTGGGAGGCCGGCACAAAAAGAAAG	1681 AATACTACTGCTAGTGACCAGATTCTGATTGAAATGCTGCCGGCCATCGGGTTT 1740
40 A0	ò 8	δ <sup>6</sup> 0	& €	& <del>8</del>	& €	& 6 	창 셤 	<i>장</i> 옵	<i>б</i> а	<i>₹</i> 0 €	ර් <u>සි</u>	<i>₹</i> ₹	<i>ò</i> €	Oy Db	λο Qu	₩ Q
APPLICATION NUMBER: US 336,672 FILING DATE: 11-APRIL-1989 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 208,997 FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:	NAME: Sholtz. REGISTRATION NUMBER: 38,615 REFERENCE/POCKET NUMBER: 4600-0093.33 TELECOMMUNICATION INFORMATION:	3 . <b>L</b>	LENGTH: 2055 Dase pairs TYPE: nucleic acid STRANDEDRES: double TOPOLOGY: linear	MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: ORF 2, MEXICO, FIGURE 7	US-07-876-941A-4 Query Match 100.0%; Score 1980; DB 2; Length 2055; Best Local Similarity 100.0%; Pred. No. 0; Match 1000.00; Constanting No. 0; Match 1000.00; Constanting No. 0; Const	GCTGTTGTTCCTCTTGTTTCTGCTATGTTGCCCGCGCA 60	Qy         61         CCGACCGGTCAGCGTCGTCGTGGGGGGGGAGGGGGGGGGG	121 TECTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	181 CCCTTTGCCCCACACGTTGCCGCTGCGTCTGGGTCTGGACCTTCGCCAACCAGCCTCCGCTTCGCCAACCAGCCTCCGCTTCGCCAACCAGCCTCCGCTTCGCCAACCTTCGCCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCGCAACGTTCCAACGTTCGCAACGTTCGCAACGTTCCAACGTTCCAACGTTCGCAACGTTCCAACGTTCCAACGTTCGCAACGTTCCAACGTTCCAACGTTCCAACGTTCCAACGTTCCAACGTTCCAACGTTCCAACGTTCAACACAACGTTCAACAACGTTCAACAACGTTCAACAACGTTCCAACAACGTTCAACAACGTTCAACAACAACAACAACAACAACAACAACAACAACAACA	241 CGGCCACTTGGCTCCACTTTGGCGACATCAGGCCCCAGGGCCCCTCGGTGCCCCCTCGCTCCCGTTGCCCCCCCC	00 - 00 - 00 - 00 - 00 - 00 - 00 - 00	361 CCGTCCCGGACGTGATTCTCGCGGTGCAATTCTACGCCGCAGTATAATTTGTCTACT 361 CCGTCCCGGAACGTGATTCTCGCGGTGCAATTCTAACGCGGCAGTATAATTTGTCTACT 361 CCGTCCCGAACGTGAATTTTTCTACGCGATTGTAATTTTGTTAATTTTTTAATTTTTAATTTTTAATTTTTAATTTTTAATTTT	421 TCACCCCTGACATCCTCTGTGGCCTCTGGCATTTAGTCCTGTATGCAGCCCCCTT		541 AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCGTTACCGGCCCCTAGTGCCTAAT [	601 GCAGTTGGAGGCTATGCTATTCTTTCTTTCTTGGCCTCAAACAACCAAC

	Db 241 CGGCCACTTGGCTACTTGGCGAGATCAGGCCCACGCCCTCCCGTGCCTCCCGTTGCC 300  301 CGACCTGCCACACGCGGGGCTGACGGCTGTGGCGCCTGCCCATGACACTCA 360  Db 301 CGACCTGCCACACGCGGGCTGCCGCTGACGCTGTGGCGCCTGCCCATGACACTCA 360  Qy 361 CCGTCCCGGACGTTGATTCTCGCGGTGAATTCTACGCCGCTGCCCATGACTTACTCTACT  Db 361 CCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCATGATAATTTGTCTACT 420  Qy 421 TCACCCTGGACGTTGATTCTGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACTT 420  Qy 421 TCACCCTGACACTCTTGTGGCTTTGGAGCTTAATTTGTCTTGTTTTATTGTCTTTTTTTT	541 AATTANGGACAGTACCGGGGCTACTANCCGTTACCGGCCCCTAGTGCCTAAT 60	Qy         721 GCATCTGAATTGGTCATCCCAAGCGAGCGCTTCACTACCGCAATCAAGGTTGGCGCTG         780           Db         721 GCATCTGAATTGGTCACCCCCCCCCCCCCCCCCCAATCAAGGTTGGCGTCG         780           CATCTGAATTGGTCAGAGCGACCCTCCCGGTCTTGTTATGCATA         840           Db         781 GTTGAGACATCTGGTGGAGCAGCACCTCCGGTCTTGTTATGCATA         840           Db         781 GTTGAGACATCTCAGTTGCTGAGCAGCACCTCCGGTCTTGTTATGCATA         840           Qy         841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCTTATTGCATA         900           Bb         941 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCTTAGGTTACTG         900           Qy         901 GACTTTGCCTTAGAGTTTCGCAATTCCACCTCTGTAACACCCATTACGGTTG         960           Db         901 GACTTTGCCTTAGAGTTTCGCAATTCTCACCACTGTAACACCCATTGTG         960           Qy         961 HCCCGTTAGAGCTTGAGGTTTCGCAATCTCACCCCTGTAACACCCAATACACGTGTG         960           Db         961 TCCCGTTACTCCAGCACTCCGCCCCCAGGGGGCCCAACGAGACTGCGGAACTGTGTG         960           Bb         961 TCCCGTTACTCCACTCCGCCCCCAAGGGGCCCAACGAATACACGCGAGCTGTG         1020           Qy         961 TCCCGTTACTCCACTCCGCCCCCAAGGGGCCCCAACGAATACACGCGGAGCTGTG         1020           Bb         961 TCCCGTTACTCCACTCCGCTCCCCCCCAAGGGGCCCCAACGAACACGAGCTGTG         1020           Bb         961 TCCCGTTACTCCACTCCGTCCCCCCCAACGCGACCCCACGCACG	OY 1021 ACCACAACTGCAGCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGGTA 1080  Db 1021 ACCACAACTGCAGCCACAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080  OY 1081 GGTGAAGTCGGCGGGGATAGCTTAACTTAACCTTGCTGACACGCTCTCGGGGTA 1080  Db 1081 GGTGAAGTCGGCGGGGATAGCTCAACATTACTTAACCTTGCTGACACGCTCCTGGG 1140  OY 1181 GGGCTCCCGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGC 1140  OY 1181 GGGCTCCCGACAGAATTTCGTCGGCTGGCGGGCAACTGTTTATTCCTCGCCCGGTT 1200
Db 1741 TCAACCTATACCACCAGGCTTGGGGGCCGGTCGCCATTTCTGCGGCGCGCGC	RESULT 5 US-08-477-292-2 Sequence 2, Application US/08477292 Sequence 10. 621641 Sequence 2. Application US/08477292 Sequence 2. Application US/08477292 Sequence 2. Application US/08477292 APPLICANT: McAtec, Patrick APPLICANT: McAtec, Patrick APPLICANT: Zhang, Yifan TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods TITLE OF ENDERS: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Cathleen M. Desjardins, M.D. STREES: 505 Penobscot Drive CITY: Redwood City STREES: CAA	COMPUTER READABLE FORM:  MEDLUM TYPE: Flappy disk  MEDLUM TYPE: Flappy disk  COMPUTER: Datentin Release #1.0, Version #1.25  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/477,292  FILING DATE:  CLASSIFICATION DATA:  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/08/327,952	FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Brookes, Allan A REGISTRATION NUMBER: 36,373 RECISTRATION NUMBER: 36,373 FERERENCE DOCKET NUMBER: G32P5 TELEPHONE: (415)369-9500 TELEFAX: (415)369-9500 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2055 base pairs TYPE: nucleic acid STRANDENNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain) US-08-477-292-2	Ouery Match  Ouery Match  Best Local Similarity 100.0%; Score 1980; DB 3; Length 2055;  Batches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 ATGCGCCTAGGCCTTTTGCTGTTTCTGCTTGTTGCCGAGGCCGCGCC 60

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                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
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CLASSIFICATION: 435
FILING DATE: 20-APRIL-1992
RIGN APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 36,672
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2055 base pairs
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NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fabian, Gary R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                              ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INDIVIDUAL ISOLATE:
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GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG
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Patent No. 6455492

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reves, Gregory R.
APPLICANT: Paudley, Daniel W.
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: T
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1381   TTTCTGTTCCGAGCAAATGATGTCCCCCCCCCCCCCCCC	RESULT 7 US-08-259-448A-2   Sequence 2, Application US/08259148A   Sequence 2, Application US/08259148A   Patent No. 5741490   GENERAL INPOWATION   APPLICANT: Bradley, Daniel W. APPLICANT: Purdy, Michael A. APPLICANT: Tur, Jr-Shin   APPLICANT: Tur, Albert W. Albert W. APPLICANT: Wardynski Karzystof Z. APPLICANT: Krawczynski Karzystof Z. APPLICANT: Krawczynski Karzystof Z. APPLICANT: Krawczynski Hepatitis E Virus Vaccine and Method (OWHER OF SEQUENCES: 60 CORRESONDENCES: 60 CORRESONDENCES: 60 CORRESONDENCES: 61 COUNTRY: USA   COUNTRY: USA   COUNTRY: USA   CONTRY: Balo Alto   STATE: CA   COMPUTER READABLE FORM: MEDION TYPE: Plopy disk   COMPUTER: Blo PC compatible COMPUTER: Blo PC compatible COMPUTER: Blot Alto   COMPU
10   CGACCTGCCAAAGCCGGGGCCTGAACGCTGTGGGCGCTGCCATGACCTCA 360   10   11   11   11   11   11   11	901 GACTTTGCCTTAGAGCTTGAGTTTCGCAATCTCACCACTGTAACACCAATACACGTGTG 960 961 GACTTTGCCTTAGAGCTTTGAGTTTCGCCAATCCACCTGTAACACCAATACACGTGTG 960 961 TCCCGTTAATCCACCACTGCTCGCTCGCCCGGGGGGCCGAGGGGCTGCGGGGCTG 1020 1021 ACCACAACTGCAGCTCACTCCTCCTCCCCCGAGGGGCCGAGGGGCTGCGGGGTG 1020 1021 ACCACAACTGCAGCCACTGCTCACTCCTCCCCCGAGGGGCCCTTAATGGGGTA 1080 1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 1081 GGTGAAGTCGCCCCAGGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 1081 GGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGCC 1140 1141 GGGTCCCCCACACATTATTCGTCGGCGCGCCACTTTATTTCCCCCCCC

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                                                                                                                                                                                                                                                                                                                                                                      NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE TOOKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MEXICO, FIGURE 7
US-08-259-148A-2
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATPORNEY AGENT INFORMATION:
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Best Local Similarity 100.
Matches 1980; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MEXICO, FIGURE
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Charle.
                                                                NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 1980; Conservative
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US-08-484-054-2
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                            1666 CGTGCCAAGCTCTCTCTTTTGGGAGGCCGGCACAAAAGCAGGTTATCCTTATAATTAT 1725
                                                                                                          1861 ACATITGAIGACTICIGCCCIGAAIGCCGCGTITAGGCCTCCAGGGIIGTGCTITCCAG 1920
                                                                                                                                                                                                                                                                                                                                                                                                                  1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGGTAAAACTCGGGAGTTGTAG 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                          1786 TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTG
                                                                                                                                                                                                                                                                                       CGTGGCAAGCTCTTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT
                                                                                  AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT
                                                                                                                                                                TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCCGCGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                         1906 ACATTICATGACTTCTGCCCTGAATGCCGCCTTTAGGCCTCCAGGGTTGTGCTTTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08484054

Patent No. 5770689

GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Pardley, Daniel W.
APPLICANT: Purdy, Mischael A.
APPLICANT: Purdy, Mischael A.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis B Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: 743.08

COMPUTE: READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: THEN PC compatible
OFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 12-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 500,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 500,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-JUNE-1989
PAROR APPLICATION DATA:
PAPLICATION NUMBER: US 336,672
FILING DATE: 11-APPLI-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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FILING DATE: 16-JUR
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4 6 A 6 A .	상 名 상 名 	8888	장 옵 장 	면 상 역 	8 8 8	G & G	\text{\tint{\text{\tin}\text{\texi}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\ti}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tin}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tin}\text{\text{\text{\text{\text{\text{\text{\text{\ti}\}\tilitht{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\texi}\text{\text{\text{\texi}\text{\text{\text{\text{\text{\text{\text{\texi}\text{\text{\texi}\text{\text{\text{\text{\text{\text{\texi}\text{\texi}\text{\texit{\	· a &	옵 상 옵 	AR US 
ORIGINAL SOURCE:   INDIVIDUAL ISOLATE: MEXICO, FIGURE 7   US-07-876-941A-2	61 CCGACCGGTCAGCCGTCTGGCCGCCGTGGGCGCGCGCAGCGGCGGTACCGGCGGTGGT 120	81 CCCTTTGCCCCAGACGTTGCCGCTGCGGGTCTGGACCTTCGCCTTCGCCAACCAGC 24	CGACCTCCCACAAGCCGGGGCTGGGCGCTGTGGCTGCCTTCGCTGCTCGTCGT	361 CCGGTCCCGGACCTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAGTTTGTCTACT 420	AATCGGCTCTGCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGACGCTCTGCCTCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGAAGAACGCTCTGCTTTGTTTTTTTT	586 AATTATCACAGTACCGGGTTGCCGGTTACCGTTTACCGGCCCTAGTGCCTTATT 645 601 GCAGTTGGAGGCTATATCCCATTTCTTTCTGGCCTCAAACAACAACCCCTACA 660	1 TCTGTTGACATGAATTCCATTACTTCCACTGATGCAGGATTCTTGTTCAACCTGGCATA	721 GCATCTGAATTGGTCATCCCAAGGGGCCCTTCACTACCGCAATCAAGGTTGGCGCTCG 780		901 GACTITGCCTTAGAGCTTGGGAATCTCACCACCTGTAACACCAATACACGTGTG 960

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1201 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATGAGGAGGAATGCTCAGCAG 1260
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226 CCCTTTGCCCCAGACGTTGCCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCC
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APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.Shin
APPLICANT: Twu, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
CLASSIPICATION ATA:
APPLICATION DATA:
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APPLICATION DATA:
FILING DATE: 17-7AN-1992
RIGN APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 505,888
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APPLICATION NUMBER: US 367,486
FILING DATE: 16-UNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNBER: US 208,997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
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REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%;
Matches 1980; Conservative 0;
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STRANDEDNESS: double
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                                                       COURTIENT LAWARE: COMMENTARY OF STREET PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
RIOR APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
RIOR APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
RIOR APPLICATION NUMBER: US 07/367,486
FILING DATE: 13-OCT-1989
RIOR APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
RIOR APPLICATION NUMBER: US 07/366,672
FILING DATE: 11-APR-1989
RIOR APPLICATION NUMBER: US 07/386,672
FILING DATE: 11-APR-1989
RAPPLICATION NUMBER: US 07/208,997
FILING APPLICATION NUMBER: US 07/208,997
FILING APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
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100.0%; Score 1980;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1980; Conservative 0; Mismatches
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    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 324-0880 TELEPAX: (650) 324-0960 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
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Patent No. 6120988

GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Kradczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Tam, Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
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ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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6497 T 1441 C 6557 C 6557 C 1501 A 1611 G 6677 G 6737 C 6737 C	SGCCGGTCCGGTCGTTTTCGGGCCGCGCGCGCGCGCGCGC	Sequence 10, Application US/09128275A  Sequence 10, Application US/09128275A  Patent No. 6229055  GENERAL INFORMATION: APPLICANT: Reyes, Gregory R  APPLICANT: Krawczynski, Krzysztof Z  APPLICANT: Tam, Albert  APPLICANT: Tam, Albert  APPLICANT: Fry, Kirk E  ITILE OF INVENTION: No. 6229005-A/No. 6229005-B Hepatitis Viral Agent  ITILE OF INVENTION: No. 6229005-A/No. 6229005-B Hepatitis Viral Agent  NUMBER OF SEQUENCES: 2  CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: CITY: Palo Alto CITY: Palo Alto CUNTRY: USA	HALLEN G KES
301 CGACCTGCCACAGGCGGCTGCGGCTGTGGCGCCTGCCCATGACACCTCA 360 5417 CGACCTGCCACAGGCGGGGCTGACGGCTGTGGCGCCTGCCCATGACACCTCA 5476 361 CCCGTCCCGGACGTGGATTCTCGCGGTGTGTGTGTGTGTG		6017 ĠACTTTĠCCTTAGAGTTTCGCAATCTCACCACCTTAACACCAATACAGTGTG 6076 961 TCCCGTTACTCCAGACTGGTCACTCCGCCCGAGGGCCGACGCGACTGTG 6076 961 TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGCCGACGGGACTG 1020 6077 TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTG 6136 1021 ACCACAACTGCAGCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 6137 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 6137 ACCACAACTGCAGCACCAGGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 6196 1081 GGTGAAGTCGGCGCGGGGATAACTTAACTTAACCTTGCTGACACGCTCCTCGGC 1140 6197 GGTGAAGTCGGCGGGGATAACTTAACTTAACCTTGCTGACACGCTCCTCGGC 6256 1141 GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGAAACTGTTTATTTCCCGCCCG	1201 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 1260 6317 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 6376 1261 GATTAAGGCTGTTGCTATCCCCCACGATTCAGTGATTCGGTGTGGTTCAGCTGGTGGTTGATTCAG 1320 6337 GATTATGACTATCCCCCACGATATCGATCTTGGTGATTCGGTGGTCATTCAG 1320 6337 GATTATGACAACCACCAGATATCGATCTTGGTGATTCGGTGGTCATTCAG 6436 6437 GATTATGACAACCAGCATGAGCAGGATCGGCCCCCCCGCGCCCTGCGCCTTCGGCCT 1380 6437 GATTATGACAACCAGCATGAGCAGGATCGGCCCCCCCCTCGCCCTCGCCCTCGGCCTTCGGCCT 6496 6437 GATTATGACAACCAGCAAGGATCGGCCCCCCCCCTCCCCCCCC

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                                  AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT
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APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/326,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
TELEPONDE: (650) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEAGH: 7171 Dasa Pairs
TYPE: nucleic acid
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Matches 1980; Conser
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Composite Mexico strain
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                  PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UUM-1988
ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615
REBERBENCE/DOCKET NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-0880
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100.0%; Score 1980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 324-0960
INFORMATION FOR SEQ 1D NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7171 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
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HYPOTHETICAL: 1
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GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Tarbough, Patrice O
APPLICANT: D
APPLICAN
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CONFINED: PELLING DATA:

APPLICATION NUMBER: US/09/553,427

FILING DATE: 07-JUN-1994

PRIOR APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1991

PRIOR APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1991

PRIOR APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1990

FILING DATE: 05-APR-1990
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APPLICATION NUMBER: US 07/367,486
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APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
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Patent No. 6379891
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5717 GCAGTTGGAGGCTATGCCTATTCTTCTGGCCTCAAACAACCACCCCTACA 5776  661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720	GACTITIGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTG   GACTITIGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTG   TCCCGTTACTCCACCACTGCTCGTCACTCCCCCGAGGGGCCCACGGGACTGCGGAGCTG   TCCCGTTACTCCACCACTGCTCGTCACTCCCCCCAGGGGGCCCACGGGACTGCGGAGCTG   TCCCGTTACTCCACCACTGCTCGTCACTCCCCCCCAGGGGGCCCACGGAGCTGCGGAGCTG   TCCCGTTACTCCAGCACTGCTCGTCACTTCACCACTTTACCGGCTTAATGGGGTA   ACCACACTGCAGCACTGCTCATCATACATTACTTACCGGCCTTAATGGGGTA   ACCACACTGCAGCACTCATCATACATTACTTACCGGCCTTTAATGGGGTA   ACCACACTGCAGCACTCATACATTACTTAACTTTACCGGCCTTTAATGGGGTA   GGTGAAGTCGCCGCGGGGGATACCTTAACTTTACCGGCCTTTAATGGGGTA   GGTGAAGTCGCCGCGGGGGATACCTTAACTTAACTTCATGAGCGTTAATGGGGTA   GGTGAAGTCGCCGCGGGGGATAACTTAACTTAACTTCCTGGCCTTTAATGGGGTA   GGTGAAGTCGCCGCGGGGGATAACTTAACTTAACTTCCTGGACTTTAATGGGGTA   GGTGAAGTCGCCACACACTGTAACATTAACTTCAATGGGGTAATGGTAATGGGTAATGGTAATAATTTCCTGCGCCGCTGGCCCGGTAATGGTAATGGTAATGGTAATAATTTCCTGGCCGCTGGCCCGGTAATGAATG	6677 GACGGGCGCCCTCCCGACTGTTGGGAATATTCCAAGACATTCTTGGCTCCCCTT 6736  1621 CGTGGCAAGCTCTCCTTTTGGAGGCCGCACAAAAGCAGGTTATCCTTATAATTAT 1680  [11

1141	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSEE: Dehlinger & Associates STREET: P.O. Box 60850 CITY: Palo Alto STATE: CA
TOTAL CONTROLLED CONTR	1018 TCCCGTTACTCCACCACCCCTCACCGCCCCCCCCCCCCC

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ORF-2 region
                                                  COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                        NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMNUMICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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99.5%;
      ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               LENGTH: 2058 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.9
Best Local Similarity 99.5
Matches 1974; Conservative
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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1 TAG 1983	1981	qa
1 TAG 1980	y 1978	٥٧
L CAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGGTAAAACTCGGGAGTTG 1980	0 1921	qa
CAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGAGAAAACTCGGGAGTTG 1977	1918	δλ
CACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTC 1920	0 1861	qa
CACACATITIGATGACTICTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTC 1917	1858	ò
TIGGCTCCACGCTCCCCTGGCTCTGCTGGAGGATACTTTTGATTATCCGGGGCGGGC	1801	qa
1 TIGGCTCCACGCCCTGGCTCTGCTGGAGGAGATACTTTTGATTATCCGGGGCGGCG 1857	1798	Qy
ATTICAACCTATACCACCAGGTTGGGGCCGGTCGGTCGCCATTTCTGCGGCCGGGGTT 1800	1741	qa
ATTICAACCTATACCACGCTGGGGCCGGTCCGGTCGCCATTICTGCGGCCGCGGTT 1797	1738	δλ
TATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCC 1740	1681	qa
1678 TATATACTACTACTACTACTACTICAATICAAAAIICGCCCGCCATCGGCCATCGGCC 1/3/		ò

Search completed: August 21, 2004, 18:11:08 Job time : 167.394 secs

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Sequence 4, Appli
Sequence 10, Appli
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Sequence 2, Appli
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Sequence 1, Appli
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Sequence 6, Appli
Sequence 14, Appli
                                                                                                               August 21, 2004, 15:15:13; Search time 885.329 Seconds (without alignments) 10985.769 Million cell updates/sec
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/ Cgn2_6/ptodata/1/pubpna/USO6_MEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO6_MEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO08_SUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO08_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-165-868-2

US-09-851-410-10

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US-09-769-066-1

US-09-769-066-1

US-09-769-066-1

US-09-851-410-6

US-10-165-868-1

US-09-851-410-6

US-10-339-090A-44

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Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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100-14-14-14-14-14-14-14-14-14-14-14-14-14-	US-10-165-868-9 US-09-769-066-5 US-09-468-147-129 US-10-319-745-129 US-10-319-745-129 US-09-468-147-193 US-09-468-147-193 US-10-319-745-195 US-10-319-745-195 US-09-468-147-192 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195 US-10-319-745-195	ALIGNMENTS R. W. W. Zysztof Z. ris E Virus & Associate: Avenue, Su.	tt compatible PC-DCS/MS-DOS in Release #1.0. TR: Un-2002 Un-2002
110 US: 110 US	nu uomoommoommom	e Krita A B B 6	FORM: Floppy disk PC compati TEM: PC-Dos entIn Relea N DATA: UMBER: US/1 N Throcan
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00000000044444000	, 4 a u u u u u u u u u u u u u u u u u u	-868-4 e 4, Application US/10165 tion No. US20030143241A1 AL INPORMATION: APPLICANT: Reyes, Gregory Bradley, Danie Twu, Ar-Shin Purdy, Michael Tam, Albert W. Krawczynski, K Krawczynski, K TITLE OF INVENTION: Hepat NUMBER OF SEQUENCES: 22 CORRESPERSEE: Deblinger STRREET: 350 Cambridg CITY: Palo Alto STRAET: CA COUNTRY: USA	ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYBE: Floppy disk COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: PATENT Relea CURRENT APPLICATION DATE: 05-Un-2002 FILING DATE: 05-Un-2002 CLASSIFICATION: APPLICATION
1315.2 1315.2 1315.2 1315.2 1314 1313.2 1301.2 1274 1274 1274 1274 1274 1274	88 90 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SULT 1 Sequence 4, Application US Publication No. US20030143: GENERAL INFORMATION: APPLICANT: Reyes, G RAPLICANT: Reyes, G TWU, JUT: PUTCH OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDR ADDRESSEE: DEL STREET: 350 CAR CITY: PAIO Alte STATE: CA COUNTRY: USA	ZI COMPUTE ME CO CO OP SO CURRENT PI
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APPLICATION NUMBER: US/07/870,985A FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
FILING DATE: 17-JAN-1990
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921

CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:

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GCAGTTGGAGGCTATGCTATATCCATTTCTTTCTGGCCTCAAACAACAACCACCATACA
                                            CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-165-868-4
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15;
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                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTATION UNDRER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1980; I; Pred. No. 0; 0; Mismatches
 FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UNNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNBER: US 208,997
                                                                                                                                                                                                                                              LENGTH: 2055 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 1980; Conservative 0;
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double near NA to mkNA SOLATE: MEXIC ID 1	Pred. No. 0;  0; Mismatches 0; In  TGCTGTTGTTCCTCTTGTTTCTGC			301 346 361	406 CCCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATATTTGTCTACT 421 TCACCCCTGACATCTCTGTGGCACTCTAGTCCTGTATTTAGTCTACT 421 TCACCCCTGACATCCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCCACTCTACT 466 TCACCCCTGACATCCTGTGGCCTCTGGCCACTATTTAGTCCTGTATGCAGCCCCCTT 466 TCACCCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCCTT	QY         481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	Qy         601 GCAGTTGGAGGCTATGCTATTCTTTCTGGCCTCAAACAACCACCCCTACA 660	721 GCATCTGAATTGGTCATCCAAGCGGCGCTTCACTACCGCAATCAAGGTTGGCGCTCG
QY         1741 TCAACCTATACCACCAGGCTTGGGGCCGGTCCCCATTCTGCCGCCGCGCTTTG         1800           Db         1741 TCAACCTATACCACCAGGCTTGGGCCGGTCCCCATTTCTGCCGCCCGC	Db 1861 ACATTIGATCATCTGCCTGAATGCCGCGTTTTAGGCTCCAGGGTTGTGCTTTCAG 1920  Qy 1921 TCAACTGCGCGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 1980  Db 1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 1980  Db 1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 1980	RESULT 2 US-10-165-868-2 Sequence 2, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION: APPLICANT: Reves, Gergory R. Bradlav, Dariol W	Twi, Jr.Shin  Furdy, Michael A.  Furdy, Michael A.  Tam, Albert W.  Krawczynski, Krzysztof Z.  TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method  NUMBER OF SEQUENCES: 22  CORRESPONDENCE ADDRESS:	ADDARSSEE: Denlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA COUNTRY: USA IP: 94306	MEDIUM TYPE: Floppy disk  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  PERATING SYSTEM: PC-DOS/MS-DOS  CURRENT APPLICATION DATA:  PAPLICATION NUMBER: US/10/165,868	TILING DATE: 00-CUN-2002  CLASSIFICATION: <unknown> PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/07/870,985A  FILING DATE: 20-APRIL-1992  APPLICATION NUMBER: US 822,335  FILING DATE: 17-JAN-1992  APPLICATION NUMBER: US 505,888</unknown>	FILING DATE: 05-APRIL-1990	ATTORNEY/AGENT INFORMATION:  ATTORNEY/AGENT INFORMATION:  NAME: Fabiar, Gary R.  REGISTRATION NUMBER: 33,875  REFERENCE/DOCKET NUMBER: 4600-0093.30  TELECHOMBY CATTON INFORMATION:  INFORMATION FOR SEQ ID NO: 2:  SEQUENCE CHARACTERISTICS:  LENGTH: 2100 base pairs  TYPE: nucleic acid

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TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
No. US20030124510A1-A/No. US20030124510H1-B Hepatitis Viral
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COMPUTER: IBM PC compatible
DERATING SYSTEM: PC-DOS/MD-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATE:

APPLICATION NUMBER: 09/128,275

FILING DATE: «Unknown»

PRILING DATE: «Unknown»

PRILING DATE: 05-APR-1991

APPLICATION NUMBER: US 07/505,888

FILING DATE: 05-APR-1990

APPLICATION NUMBER: US 07/420,921

FILING DATE: 13-0CT-1989

APPLICATION NUMBER: US 07/367,486

FILING DATE: 11-APR-1989

APPLICATION NUMBER: US 07/36,672

FILING DATE: 11-APR-1989

APPLICATION NUMBER: US 07/36,672

FILING DATE: 11-APR-1989

APPLICATION NUMBER: US 07/208,997

FILING DATE: 17-UIN-1988

ATTORNEY/AGENT INFORMATION:

NAME: PELILON: JOANNE R.

REGISTRATION NUMBER: 42,995

REFERENCE/DOCKET NUMBER: 4600-0183.24
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STRANDEDNESS: Composite Mexico strain
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite;
CITY: Palo Alto
STATE: CA
COMTRY: USA
ZIP: 94306
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APPLICATION NUMBER: US/09/851,410
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                                                                                                                      APPLICANT: Reyes, Gregory R
Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof
Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-851-410-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-May-2001 PRIOR APPLICATION DATA:
                                 Sequence 10, Application US/09851410 Publication No. US20030124510A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7171 base pairs
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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Best Local Similarity
Matches 1980; Conserv
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                      US-09-851-410-10
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ORGANISM: Hepatitis E Virus Mexico(M74506) -10-239-090A-49 Query Match Best Local Similarity 100.0%; Fred. No. 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  ATGCGCCTAGGCTTTTGCTGTTTTCTTTGTTTTGTTTT		TICHGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGGGCCCCTCCGCTGCTCCCGTCGC 30 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGGCGCCCTCCGCTGCTCCCGTCGC 30 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGCGCCCTCCGCTGCCTCCGTCGC 54 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCTGCCCTCCGCTGCCTCCCTC			AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC		5717 GCAGTTGGAGGCTATGCTATATCCATTCTGGGCCTCAACACAACAACCCCTACA 5776 661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGATTCTTGTTCAACCTGGCATA 720	721 GCATCTGAATTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCG 780 	181 GTTGAGACATCTGGTGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATA 840	5957 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACGGTGCCCTTGGCTTACTG 6016 901 GACTTTGCCTTAGAGCTTGGGAATCTCACCACCAGTAACACCAATACACGTGTG 960

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                                    TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
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                                                                                                                                           ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFCATION: cURKNOWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/542,634
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1957.4; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: Hepatitis E Virus
ORF-2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
  McAtee, C. Patrick
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
               Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2058 base pairs
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McAter,
Yarbough, Parran, Yifan
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INFORMATION FOR SEQ ID NO: 2:
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ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1974; Conserv
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                                                                                                                                                                                                                                                         Length 1647
                                                                       LENGE CHARLE 1647 base pairs
LENGTH: 1647 base pairs
TYPE: nucleic acid
STRANDEDNESS: Hepatitis E virus (Mexico strain)
r62kDa, FIGURE 2
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                         DB 9;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
HYPOTHFTICAL: NO
ONLGINAL SOUNCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
TELECOMMUNICATION INFORMATION
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         81.9%;
                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          Matches 1638; Conservative
                                                                                                                                                                                                                                                                          Similarity
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 1441 GACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTG
                                 GTGAATGTTGCGACTGGCGCGCGGTAGCCCGATCGCTTGACTGGTCCAAAGTCACC
                                                    CTCGACGGGGGGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Yarbough, Patrice O. Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/769,066 FILING DATE: 24-Jan-2001
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fuerst, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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US-09-769-066-4
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                                                                                                                 Length 1990;
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                                                                                                             69.3%; Score 1371.8; DB 13; Lengt
81.1%; Pred. No. 0;
ive 0; Mismatches 372; Indels
                                                              E virus
                                                                                                             Query Match 69.3
Best Local Similarity 81.1
Matches 1608; Conservative
                         ; LENGTH: 1990
; TYPE: DNA
; ORGANISM: hepatitis
US-10-381-770-5
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US-10-381-770-5
US-10-381-770-5
; Sequence 5, Application US/10381770
; Publication No. US20040052813A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPRISING SAID FRAGMENT OF HEBATISIS E VIRUS, THE VACCINE COMPOS
TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
TITLE OF INVENTION: US/10/381,770
CURRENT APPLICATION NUMBER: US/10/381,770
; CURRENT FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
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TYPB: nucleic acid
STRANDEDNESS: Hepatitis E Virus (Burma strain)
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
PLLING DATE: 24-Jan-2001
CLASSIFICATION: <u >u</a>, <u >u</a>, <u >u</a>
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APPLICATION NUMBER: 08/542,634

FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0293.30

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (415) 324-0880
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Pred. No. 0;
0; Mismatches
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ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
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(15) 324-0960
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MEDIUM TYPE: Floppy disk
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ULE TYPE: DNA (genomic)
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llarity 81.0%;
Conservative
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STATE: CA
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Best Local Simi
Matches 1606;
RESULT 8
US-09-769-066-1
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                              APPLICATION NUMBER: US/07/870,985A
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                                                        FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JNN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1999
APPLICATION NUMBER: US 420,921
FILING DATE: 11-OCTOBER-1999
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
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FILING DATE: 11.APRLL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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NO: B
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SEQUENCE DESCRIPTION: SEQ ID
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SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                   CLASSIFICATION: <Ui
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Best Local Similarity
Matches 1606; Conserv
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             FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UDNS-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
TELEOROWINICATION INFORMATION:
TELECRANICATION INFORMATION:
TELEPRAK: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

69.1%; Score 1368.6;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1606; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-165-868-1
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APPLICANT: Rever, Gregory R.

Twu, Jr-Shin

Purdy, Michael A.

Tam, Albert W.

Krawczynski, Krzysztof Z.

TITLE OF INVENCH Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: OMTA:
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 105-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
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Publication No. US20030143241A1
GENERAL INFORMATION:
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Qy         1798 TTGGCTCCACGCTCCGCCTGGCTGGAGGATACTTTTGATTATCCGGGGCGGGC	NUMBER OF STEAM OF SECURATION OF A PARTICULAR SECURATION OF SECURATION O	TYPE: nucleic acid
721 GCATCTGAATTGAATTGAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 765 721 GCATCTGAATTGGACATCCCAAGCGACGCCTTCACTACCGCAATCAAGGTTGGCGCTC 780 721 GCATCTGAGCTTGTGATCCCAAGTGAGCGCCTTCACTATCGTAACGTTGCGTCC 825 781 GTTGAGACATCTGGTTGCTAGCAGGAGACCCCTCCGGTTGTCATGTTATGCATA 840 826 GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACTCTGGTTATGCATA 845 827 GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACTCTGGTTATGCATA 845 828 GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACTCTGGTTTATGCTTTGCATA 845 841 CATGGCTCTCCAGTTAACTCCTATACCCATTATCCGGTGCCCTTGGCTTGCTG 945 846 CATGGCTCATAACTCCTATACTAATACCACTATACCGGTGCCCTCGGCTGTTG 945 847 GTCTTTGCCTTAAGGTTTGCAATTACTCACTATACCGGTGACCTCGGGCGGG	Trecognate and the control of the	Db 1786 ATTICCACTTACACCACTAGCCTGGGTGCTGCCGTCTCCATTTCTGCGGTTGCGTT 1845

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                                                                              5987 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
                                                                                                      GACITIGCCTIAGAGCIIGAGIIICGCAAICICACCACCIGIAACACCAAIACACGIGIG
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0; Mismatches
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  strain
                                                                                                                                           NAME/KEY: CDS
LOCATION: 5106..5474
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                       5147..7126
STRANDEDNESS: HEV -
                                                                            CDS
28..5106
         TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
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                         GACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTG
                                               GACCAGACTACGTATGGGTCCACCAACCCTATGTATGTCTCCGACACAGTCACGCTC
                                                                       GTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCCGATCGCTTGACTGGTCCAAAGTCACC
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Sequence 164, Application US/09468147A

Publication No. US20030049601A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Schlauder, George G.

APPLICANT: Desai, Suresh M.

APPLICANT: Desai, Suresh M.

APPLICANT: Desai, Suresh M.

APPLICANT: Desai, Suresh M.

APPLICANT: Manbanar, I. K.

TITLE OF INVENTION: HEPATITIS E VIRUS

TITLE OF INVENTION: HEPATITIS E VIRUS

TITLE OF INVENTION: HEPATITIS E VIRUS

TITLE APPLICATION NUMBER: US/09/468,147A

CURRENT FILING DATE: 1999-12-21

SEALIER FILING DATE: 1999-10-15

EARLIER FILING DATE: 1999-10-15

EARLIER FILING DATE: 1999-10-15

SERLIER FILING DATE: 1999-10-15

SERLIER FILING DATE: 1997-10-15

NUMBER OF SEQ ID NOS: 258

SOFTWARE: PastSEQ for Windows Version 3.0

SSEQ ID NO 164
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                                                                        CCCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT
                                                  CCCTTTGCCCCAACGTTGCCGCTGCGTCCTGGACCTCGCCTTCGCCAACCAGCC
                          Gaps
 Length
                          Indels
 DB 10;
                          406;
Score 1315.2;
Pred. No. 0;
3; Mismatches
  66.4%;
                Best Local Similarity 79.2
Matches 1570; Conservative
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APPLICANT: Abbott Laboratories
                 APPLICANT: Schlauder, George
APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Hepatitis E Virus
                                                                                                                                                                                                                                                                    OTHER INFORMATION: us2full
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Best Local Similarity 79.2
Matches 1570; Conservative
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GTAGGTGAAGTCGGCGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTC
                                                       GTTGGTGGGTGGGTGTGTTCGCCCTGACACTGTTCATCTCGCTGATACGCTTCTC
                                                                                GTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAG
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Sequence 165, Application US/09468147A Publication No. US20030049601A1 GENERAL INFORMATION:

120 301 CGACCTGCCACAGCCGGGGGCTGCGCTGTGGGGCGCCTGCCCATGACACCTCA 360 5197 AIGCGCCCTAGGGCTGTTCTGTTGCTCTTCGTGCTTTTGCCTATGCTGCCCGCGCCA CCGACCGGTCAGCCGTCTCGTCGTGGGCGGCGCAGCGGTGGTACCGGCGGTGGT CCCTTTGCCCCAGACGTTGCCGCTGCGGTCTGGACCTCGCCTTCGCCAACCAGCC 5377 cccrirceccacardrogrrrcacaacccagagagagagacrosccricaacaacccc 241 CGGCCACTIGGCTCCACTIGGCGAGATCAGGCCCCAGCGCCCCTCCGCTGCCTCCCGTCGC DB 10; Length 7277, ٠<u>,</u> JOTHER INFORMATION: 0xf1

FEATURE:

INAME/KEY: CDS

OTHER INFORMATION: 0xf1

FEATURE:

INAME/KEY: CDS

OTHER INFORMATION: 0xf2

OTHER INFORMATION: 0xf3 at positions 5159-5527

OTHER INFORMATION: Xaa = Unknown or Other at position 332

OTHER INFORMATION: Xaa = Unknown or Other at position 448

OTHER INFORMATION: Xaa = Unknown or Other at position 448

OTHER INFORMATION: Xaa = Unknown or Other at position 634

OTHER INFORMATION: Xaa = Unknown or Other at position 634

OTHER INFORMATION: Xaa = Unknown or Other at position 634

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OTHER INFORMATION: Xaa = Unknown or Other at position 1591

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OTHER INFORMATION: Xaa = Unknown or Other at position 1938

OTHER INFORMATION: Xaa = Unknown or Other at position 1938

OTHER INFORMATION: Xaa = Unknown or Other at position 1938

OTHER INFORMATION: Xaa = Unknown or Other at position 1938

OTHER INFORMATION: Xaa = Unknown or Other at position 1938 APPLICANT: Desail, Calcon. 1.
APPLICANT: Mushahwar, I. K.
ITILE DE INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 623-US.Pl
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT APPLICATION NUMBER: US 09/173,141
EARLIER FILING DATE: 1998-10-15
EARLIER PILING DATE: 1998-10-15
EARLIER PILING DATE: 1998-10-15
EARLIER FILING DATE: 1998-10-15
SOFTWARE: FALSO DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FASESEQ for Windows Version 3.0
: SEQ ID NO 165 66.4%; Score 1315.2; 79.2%; Pred. No. 0; ive 3; Mismatches ð 임

1438	Db 6637 GACCAGACTACGT Oy 1498 GTGAATGTTGCGF	Db 6697 GTTAATGTGGCTF Oy 1558 CTCGACGGGGGG	6757	6817	6877		6997	7057	OV 1978 TA 1979	7117	Search completed: August 2 Job time : 893.329 secs							
		421 TCACCCCTGACAICCTCTGGGCACTCTGGCACTAATTTAGTCCTGTATGCGGCCCCCTT 480	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	541 AATTATGCACAGTACCGGGTACTACTATCCGTTACCGGCCCTAGTGCCTAAT 600	601 GCAGTIGGAGGCTATGCTATATCCATTTCTGGCCTCAAACAACCACAACCCCTACA 660 	661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720 	721 GCATCTGAATTGGTCATCCCAAGCGAGGCGTTCACTACCGCAATCAAGGTTGGCGCTCG 780 	781 GTTGAGACATCTGGTGTTGCTGAGGAGGAGCACCTCCGGTCTTGTCATGTTATGCATA 840	841 CATGGCTCTCCAGTTAACCCTTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG 900	901 GACTITIGCCTIAGAGCTIGAGATTICGCAATCTCACCTGTAACACCAATACACGTGTG 960 	961 TCCCGTTACTCCAGCACTGCTCACATCCGCCCGAGGGGCCGACGGGACTGCGGAG 1017	1018 CTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGG 1077	1078 GTAGGTGAAGTCGGCGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTC 1137	1138 GGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGCAACTGTTTATTCCCGCCCG	1198 GITGICICAGCCAAIGGGAGCCAACGGGAGCICIAIAACAICAGIGGAGAAIGCICAG 1257 	1258 CAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATT 1317 	1318 CAGGATTATGACAACAAGGATGAGCAGCCCACCCCGTCGCGCGCCATCTCGG 1377	1378 CCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCGAGTAT 1437 
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TTACGGGTCGTCAACTGGCCCGGTTTATATCTCCGGACAGCGTGACTTTG 1497 GCTCTCCTTTTGGGAGGCCGGCACAACAAAGCAGGTTATCCTTATAAT 1677 rgacrrcrgcccrgaargccgcgcrrrraggccrccagggrrgrgcrrrc 1917 TGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCC 1737 TACCACCAGGCTTGGGGCGGTCCGGTCGCATTTCTGCGGCCGCGGTT 1797 

21, 2004, 22:42:05

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 16, 2004, 13:02:51; Search time 57 Seconds (without alignments) 3271.603 Million cell updates/sec Run on:

US-09-851-410A-8 3408 Perfect score:

1 MRPRPILLLLLMFLPMLPAP......OSTVAELQRLKMKVGKTREL BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

99

1586107 seqs, 282547505 residues

1586107 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04;\*
1: geneseqp1980s;\*
2: geneseqp21090s;\*
4: geneseqp2001s;\*
5: geneseqp2001s;\*
6: geneseqp2003s;\*
7: geneseqp2003bs;\*
8: geneseqp2004s;\* geneseqp1990s: \*
geneseqp2000s: \*
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geneseqp2003ss: \*
geneseqp2003bs: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aar18785 HEV OBE2		Henati		, _				, σ	٠.			Henatiti										, ,			STITUTE DESCRIPTION
SUMMARIES	ID	AAR38785	AAR39306	AAR96089	AAW35826	AAW80197	AAW93389	AAB24120	AAB62523	AA015699	ADD24376	AAW76369	AAW71210	AAR70323	AAR91814	AAW93386	ABB81670	ADA50060	ADB97807	ABJ04803	AAE12980	AARS1265	AAW81520	AAWGA3GG	AAWG3388	AB,104811	1
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## ALIGNMENTS

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Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
                                                                            Location/Qualifiers
         AAR38785 standard; protein; 660 AA.
                                                                  Hepatitis E virus; Burma strain.
                                                                                                   613. .660
/label= 406.3-2
                                                                                225. .660
/label= C2
334. .660
/label= SG3
                                       (first entry)
                             (revised)
                                               HEV ORF2 protein.
                            24-OCT-2003
25-MAR-2003
11-JAN-1994
                   AAR38785;
                                                                           Key
Peptide
                                                                                          Peptide
                                                                                                   Peptide
RESULT 1
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WO9314116-A1 22-JUL-1993.

93WO-US000459. 15-JAN-1993;

92US-00822335. 92US-00876941. 17-JAN-1992; 01-MAY-1992;

(GENE-) GENELABS TECHNOLOGIES INC. (USSH ) US SEC DEPT HEALTH.

Carl Tam AW, Reyes GR, Bradley DW,

Σ

WPI; 1993-243144/30. N-PSDB; AAQ47129.

New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1, ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.

Disclosure; Fig 8; 48pp; English.

Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1, ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to

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92US-00822335.
                            93WO-US000475
                                                                                                                                                                                                                                Sequence 660 AA;
                             19-JAN-1993;
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prevent infection by HEV. The antibodies can neutralise and block HEV infection and can be used to prevent or treat HEV infection. The peptides and antibodies can also be used as diagnostic reagents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                             VGEIGRGIALTENLADTLIGGLPTELISSAGGOLFYSRPVVSANGEPTVKLYTSVENAQ
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                                                                                                     PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
                                                                                                                                    PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                                                                                                               NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
                                                                                                                                                                                             MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN
                                                                             Gaps
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                                                             Score 3408; DB 2;
Pred. No. 5.3e-263;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain HEV ORF2 puative virus
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                                                                               Conservative
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                                                                 Query Match
Best Local Similarity
Matches 660; Conserv
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                                                 Sequence 660 AA;
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14-FEB-1994
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C-terminal or
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                                               AW,
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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               DEPT HEALTH & HUMAN SERVICES
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derived from capsid
GENELABS TECHNOLOGIES INC
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                                                 Twu J,
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                                                 DW,
                                                                                                                                 Antigen and antibody contain peptide(s) de against protein.
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N-PSDB; AAQ46813.
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E virus; Burma; Mexico; immunoassay; peptide antigen; antibody; HEV.
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                                                                                                                            DFALELEFRNITPGNTNTRVSRYSSTARHRIRRGADGTAELTTTAATRFMKDLXFTSTNG
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                  NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
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                                                                              QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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89US-00367486.
89US-00420921.
90US-00505888.
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92US-00822335
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92US-00876941
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N-PSDB; AAT96959.
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01-MAY-1992
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                                                                                                                                                                                                            HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
                                                                                                                                                                                      Hepatitis E virus (Burma strain) capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 78-80; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Yarbough PO,
                                                                                                             AAR96089 standard; protein; 660 AA
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95US-00542634.
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13-OCT-1995;
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06-AUG-1996
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                                                        A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents the protein from the open reading frame, ORF2, from HEV Burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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       Diagnosis of hepatitis E virus Burma and Mexico strain infection immunoassay with hepatitis E virus peptide antigens.
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
                                                 Col 39-42; 36pp; English
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Matches 660; Conserv
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                                                  Disclosure;
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AAW80196-98 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (BT-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF1 sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-2003 to correct OR field.)
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                                                                                    non B hepatitis virus; ET-NANB;
HEV isolate; vaccine; diagnostic probe.
                                                                                                                                                                                                                                                                                                                                                                   Yarbough
                                                        Protein encoded by ORF2 of ET-NANB (HEV) Burma strain DNA sequence
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100.0%; Pred. No. 5.3e-263;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   Krawczynski KZ,
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Burma
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00505888.
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                                                                                     Enterically transmitted
Hepatitis E virus; HEV;
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                                                                                                                                Non-A.
non-B hepatitis virus.
                        (revised)
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25-JUL-1994;
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AAW80197 standard; protein; 660

RESULT 5 AAW80197

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mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both
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0
                                                             ; Score 3408; DB 2;
; Pred. No. 5.3e-263;
0; Mismatches 0;
experimentally and clinically without fear of
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                                                                                      Matches 660; Conservative
                                                                          Similarity
                                    Sequence 660 AA;
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(GENE-) GENELABS TECHNOLOGIES
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89US-00336672.
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94US-00279823.
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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89US-00336672.
89US-00420921.
90US-00505888.
91US-00681078.
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                                95US-00478507
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Best Local Similarity 100.
Matches 660; Conservative
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25-JUL-1994;
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13-OCT-1989;
                                07-JUN-1995;
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11-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterically transmitted nonA/nonB viral hepatitis agent; viral;
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These

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Sequence 660 AA;
                                     17-JUN-1988;
11-APR-1989;
16-JUN-1989;
                    19-APR-2000;
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05-APR-1990;
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                                                              Query Match 100.0%; Score 3408; DB 4; Best Local Similarity 100.0%; Pred. No. 5.3e-263; Matches 660; Conservative 0; Mismatches 0;
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                            DNA sequence from HEV-Burma strain
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strain; bile; ORF2.
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The invention comprises a method for detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a sample and isolating HEV agents or nucleic acid fragments produced by the agent. The method utilises PCR - using bile from a human or cynomolgus monkey actively infected with HEV as a source of the agent. The method of the invention is used for detecting the presence of a viral agent in a sample of cultured cells infected with the agent and isolating enterically transmitted nonA/nonB HEV agents or nucleic acid fragments produced by the agent. The present amino acid sequence represents the protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated from a Burmese strain of the Hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 nonA/nonB hepatitis
humans and monkeys using
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100.0%; Pred. No. 5.3e-263;
iive 0; Mismatches 0;
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                                                    88US-00208997.
89US-00336672.
89US-00367486.
89US-00420921.
9UUS-00681078.
94US-00679833.
2000US-00553427.
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Best Local Similarity 100.
Matches 660; Conservative
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Length 660;
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Score 3408; DB 7;
Pred. No. 5.3e-263;
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Query Match 100.

Best Local Similarity 100.

Matches 660; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis
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   QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                      QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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89US-00336672.
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9UUS-00505888.
91US-00681078.
94US-00279823.
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16-JUN-1989;
13-OCT-1989;
05-APR-1990;
05-APR-1991;
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Hepatitis
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                                              Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation.
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                                                                                                          This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HBV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HBV than
                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                      1 MRPRPILLLLLIMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFALPYIHPTN
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                                                                                                                                                                                                     Length 660;
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                                                                                                                                                                                                    Score 3401; DB 2;
Pred. No. 1.9e-262;
                                                                                                                                                                                                                        0; Mismatches
  EISEI KENKYUSHO.
                                                                                        Claim 13; Page 24-26; 29pp; Japanese
                                                                                                                                                                                                   99.8%;
                                                                                                                                                                                                            Local Similarity 99.8
les 659; Conservative
KOKURITSU YOBO
                   WPI; 1998-535037/46
                                                                                                                                                            previously possible
                              N-PSDB; AAV61688
                                                                                                                                                                                Sequence 660 AA;
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AAW71210 standard; protein; 660 AA

RESULT 12
AAW71210
ID AAW7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW71209-11 represent the proteins encoded by the open reading frames (ORFs) of the DNA sequence of the Burmese isolate of an enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid sequence may be used for identifying and sequencing the entire viral sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV), detecting ET-NANB in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in vaccines. (Updated on 25 MAR-2003 to correct PF field.)
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                                                                                                         transmitted nonA/nonB hepatitis virus; identification; HEV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN
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                                                              Protein encoded by ORF 2 of the Burmese isolate of ET-NANB
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99.8%; Pred. No. 1.9e-262;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KZ,
                                                                                                                                                                                                                                                          /note= "not specified"
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                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-00336672.
89US-00367486.
89US-00420921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00505888
91US-00681078
                                                                                                                        ET-NANB; detection; vaccine
                      (first entry)
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  (revised)
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                                                                                                                                                                       Hepatitis virus
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13-OCT-1989;
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25-MAR-2003
                    30-0CT-1998
                                                                                                         Enterically
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Length 660;

DB

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RNA from an HEV strain isolated in the Xinjiang region of China was subjected to RT-PCR to obtain fragments corresp. to ORP2 (given in AAQ86592) and ORP3 (AAQ86593) that encoded antigenic proteins (AAR70323-24, respectively). DNA fragments were manipulated into pGEX vectors for production of GST fusion proteins in E. coli. Applications include HEV infection diagnosis, therapy and vaccine development. (Updated on 25-WAR-2003 to correct PN field.)
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ASELVI PSERLHYRNQGWRSVETSGVAEBEATSGLVMLCIHGSLVNSYTNTPYTGALGLL
                                          VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ
                                                                                                                                  QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                                                                                                                                                                 DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                                                                                               LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                             LAPHSALALLEDTLDYPARAHTPDDFCPECRPLGLQGCAFQSTVAELQRLXWKVGKTREL
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                                                                                                                   QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                       DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigens of hepatitis E virus (HEV) - selectively immuno:reactive convalescent and/or acute phase circulating antibodies to HEV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEV; ORF2; antigen; vaccine; immunogen
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93AU-00002964
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                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1994;
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28-SEP-1995
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Sequence 660 AA;

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                                                                PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enteric transmission;
antibody; vaccine; immunisation;
                                                                            DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                                                                                                                                                                                                                                  LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                                                                                                                                                     LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
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                                                                                                   PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                                                                                     NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
                                                                                                                                                                    ASELVI PSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL
                                                                                                                                                                                                                                                                          QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                                 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIN
                 ö
                  Indels
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        2.8e-262;
Score 3399; DE Pred. No. 2.8e-1; Mismatches
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antigen; detection;
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 99.78;
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 Query Match
Best Local Similarity 99.7
Matches 658; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E virus;
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The present sequence is the protein prod. of ORF-2 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue, using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SBS-PAGE of cell lysaces of insect cells infected with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781 Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection. DEPT HEALTH & HUMAN SERVICES. 6; Page 13-15; 121pp; English. 1996-209320/21 WPI; 1996-20932U/ N-PSDB; AAT27394 Sn (HSSn) Tsarev SA, Claim NAME OF COLORS OF STATES O

Sequence 660 AA;

Gaps ·, 99.5%; Score 3391; DB 2; Length 660; 99.4%; Pred. No. 1.2e-261; Indels 3; 1; Mismatches Local Similarity ... Query Match Matches

1 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFALPYIHPTN

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180 PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI 121 181

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180 240 240

> NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 241 181

VGBIGRGIALTLENLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 361 361 421

DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 421 481 481

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540 540 009 600

LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL 660 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 541 601

LRGKLSFWEAGTIKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV

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999 601

RESULT 15 AAW93386

9 AAW93386 standard; protein;

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AAW93386;

(first 11-JUN-1999

Human HEV ORF 2 protein from strain

Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy; vaccine; immunise; infection; detection; diagnosis; prevention.

Hepatitis E virus.

WO9904029-A2

28-JAN-1999

98WO-US014665. 17-JUL-1998;

97US-0053069P

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Purcell RH; Emerson SU, Meng X,

WPI; 1999-132270/11.

New isolated swine hepatitis E virus - used to develop products for th diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans.

Example 1; Fig 3A; 70pp; English.

mutants which are capable of cross reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can also be used as a therapeutic treatment for infection by other arrains of HEV. The swine HEV can also be used as a therapeutic treatment for infection by other antibodies which can be used in therapy, detection by other products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or This invention describes a swine hepatitis E virus (HEV) and its natural contamination 

Sequence 660 AA;

360 420 420

Gaps . Length 660; 3; Indels 99.5%; Score 3391; DB 2; 99.4%; Pred. No. 1.2e-261; 1; Mismatches al Similarity 99.4 656; Conservative Query Match Best Local S: Matches 656

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1 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFALPYIHPTN

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480 480 PVPDVDSRGAIIRRQYNLSTSPLISSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180 

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181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI 240

240 300 300	360 360	420	480	540 540	600	960	
NYAQYRVARATIRYRPLYPNAVGGYAISISFWPQTITIFISYDWNSIISIDVKLUVÇFGI ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 	DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATREFMKDLYFTSTNG	VGEIGRGIALTLENLADTLLGGLPTELISSAGGOLFYSRPVVSANGEPTVKLYTSVENAQ 	ODKGIAIPHDIDLGESRVVIQDYDNQHEQDRFTPSPAPSRPFSVLRANDVLWLSLTAAEY	DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 	LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV	1 LAPHSALALLEDTI.DYPARAHTFODFCPECRPIGLOGCAFOSTVAELORLKWKVGKTREL	
241	301	361	421	481	541	601	
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Search completed: August 16, 2004, 13:33:47 Job time : 59 secs

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	Copyright

- protein search, using sw model OM protein

August 16, 2004, 13:28:02; Search time 20 Seconds (without alignments) 3174.320 Million cell updates/sec Run on:

US-09-851-410A-8 3408 1 MRPRPILLLIAMILPMLPAP......QSTVAELQRLKMKVGKTREL

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 0B 0B Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
2: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

St	Description	structural protein			probable RTX famil			Q	hemagglutinin-like	hemagalutinin-like	hemagalutinin-like	hypothetical prote			д	probable membrane	flocculation prote		hypothetical prote	glucan 1,4-alpha-q	probable exported	hypothetical prote		hypothetical prote		glucan 1.4-alpha-g	ABC transporter. H	L2 profein - himan	probable membrane	tail fiber protein
SUMMARIES	ID	VHWWH2	B44212	S55862	B85547	F90696	T45025	\$52863	E82750	E82589	B82519	T21460	S69703	S67571	S59310	S57180	S53465	AB0480	F75477	S48478	AB0821	T02759	JC5062	S51959	JU0474	ALBYG	B87673	P2WL47	T02852	T14650
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127.5	127	127	126.5	126.5	126.5	126	125.5	125.5	125.5	124	124	124	123.5	123	122.5

## ALIGNMENTS

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nepatitis E virus (strain Burma)

C;Species: hepatitis E virus
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C;Species: nepatitis E virus
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 23-Jul-1999
C;Accession: C4077B
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A4077B; MUID:92024067; PMID:1926770
A;Accession: C4077B
A;Molcoule type: genomic RNA
A;Residues: 1-660 < TAM>A;Residues: 1-660 < TAM>A;Cross-references: GB:M7321B; NID:9330023; PIDN:AAA45736.1; PID:9330026
A;Cross-references: GB:M7321B; NID:9330023; PIDN:AAA45736.1; PID:9330026
C;Superfamily: hepatitis E virus structural protein 2
C;Reywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-660/Product: structural protein 2 #status predicted <SIG>

Gaps .. 0 Length 660; Indels 100.0%; Score 340%; DB 1; 100.0%; Pred. No. 8.2e-208; tive 0; Mismatches 0; 660; Conservative Local Similarity Query Match Best Loca Matches

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120 9 9 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 1 MRPRPILLLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN 61 ਨੇ g à

120 180 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 19 121 qq ò

180 121 PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS g

240 240 181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI q ò

300 DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360 DPALELEERRNI,TPGNTNTRVSRYSSTARHRI,RRGADGTAELTTTAATRFWKDLYFTSTNG 360 301 301 à g

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Db 480 DGSTYGSSTGPVYISDSVTLANVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLP 539  Cy 541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600	RESULT 3 SSEGE2 probable membrane protein YML327w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein N0320 C;Species: Saccharomyces cerevision 03-Nov-1995 #text_change 21-Jul-2000 C;Species: Saccharomyces cerevision 03-Nov-1995 #text_change 21-Jul-2000 C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000 C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000 C;Accession: S55862, S63308; S51288 R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C. A;Reference number: S55859; MUID:95373280; PMID:7645347 A;Reference number: S58629; MUID:95373280; PMID:7645347 A;Reference number: S58629; MUID:9633655; PIDN:CAA86371.1; PID:g633659 R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C. Submitted to the Protein Sequence Database, April 1996 A;Rocession: S63308 A;Rocession: S63308 A;Rocession: S63308 A;Rocession: S6308 A;Rocess	Query Match         4.2%;         Score 143;         DB 2;         Length 1041;           Beef Local Similarity         20.4%;         Proceed, No. 0.40;         Maches 131;           Matches 144;         Conservative 94;         Mismatches 238;         Indels 230;         Gaps 31;           Qy         48         SQPPAIPYIHPTNPPAPDVTAAAGAGPRVRQPARPLGSAWRDQACRADASKRRPTT 104         104           Db         340         SQSSAIPEVAVTASLSSGILSSTVDGASTSDABASWAVTVSS 382           Qy         105        AGAAPLTAVAPAHDTPPVPDVDSRGAILRRQVNLSTSPLTSSVATGTNLLYARPL 160           Db         383         SSEQASSSISLSAPSSNSTPTTPSSSLATETYSISSASI 425           Qy         161         SPLLPLQDGTNHHIMATEASNYAQXRVARATIRKRPLVBNAVGGYALSISFWPQTT 217           Db         426         SVTQASYIDNSTTTAATRGSTSTIAVSSAEKLSSTLSYTSNVTISVSSATQHT 478           Qy         218         TPTSVDMNSTTTAATRGSTSTLYRRQGMESVTEGVABEEATGLWW 277           Db         479         TPSXVS-NNTTLSSSSUL
QY         421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480           Db         421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480           QY         481 DQSTYGSSTGDVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           Db         481 DQSTYGSSTGDVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           Db         481 DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           QY         541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600           Db         541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTTTSLGAGPVSISAVAV 600	LAPHSALALLEDTLDYPARAHTFDDFCPECRFLGLQGCAFQSTVAELQRLKMKVGKTREL 660  LAPHSALALLEDTLDYPARAHTFDDFCPECRFLGLQGCAFQSTVAELQRLKMKVGKTREL 660  LAPHSALALLEDTLDYPARAHTFDDFCPECRFLGLQGCAFQSTVAELQRLKMKVGKTREL 660  patitis E virus  b-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999  b-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999  s-44412  s-60-558, 1992  cular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE cular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE cular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE cular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE cular laptocein control contro	

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oy Op	468 NDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVAR 512	රු අ	491 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSF- 547 2866 PAGTAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTASVTNAQGNSSTA 2923
<b>상</b> 원	513 SLDWTKVTLDGRPLSTIQ	දු දු	548WEAGTTKAGYPYNYTTASDQLLVENAAGHRVAISTYTTSLGAG 591  2924 SHNVQVNTALPGITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968
oy en	545 LSFWEAGTTKAGYPYNYNTTASDQLLJVENAAGHRVAISTYTTSLG 589    :	RESULT :	S
oy Db		hypother C;Specie C;Date: C;Acces	ical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RI 8s: Escherichia coli 18-Jull-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 sion: F90696
RESULT B85547 probabl C;Speci	a 0157:H7, substrain	R; Hayasi gasawara gasawara DNA Res A; Title A; Refere A; Access	11, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; Complete genome sequence of enterohemorrhaqic Escherichia coli O157:H7 and genomice number: A99629; MUID:21156231; PMID:11258796
C; Date C; Acce: R; Pern; iller, Nature A; Title	ce_revision ib-reb-2001 #text_change 14-Sep-2001 , G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, enterohemorrhagic Escherichia coli 0157:H7. MUID:21074935; PMID:11206551	A;Status A;Molecu A;Residu A;Cross- A;Experi C;Geneti A;Gene:	A,Status: preliminary A,Molecule type: DNA A,Mescule type: DNA A,Residues: 1-5291 <hay> A,Cross-references: GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:GN00154 A,Experimental source: strain O157:H7, substrain RIMD 0509952 C,Genetics: Accessed to the control of the cont</hay>
A; Molec A; Molec A; Resic A; Cross	PDB. CMODIAE. ITMCD. 706	Query Ma Best Loc Matches	Query Match Best Local Similarity 22.3%; Pred. No. 8.2; Matches 131; Conservative 70; Mismatches 235; Indels 151; Gaps 28;
A, Exper C, Genet A, Gene		à q	60 NPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAA 108 
Quer) Best Match	Query Match 4.1%; Score 139.5; DB 2; Length 5188; Best Local Similarity 22.3%; Pred. No. 8; Matches 131; Conservative 70; Mismatches 235; Indels 151; Gaps 28;	ò 8	109 PLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQD 168 
Qy Dp	60 NPFAPDVTAAAGAGPRVROPARPLGSAWRDQAQRPAVASRRRPTTAGAA 108	<i>ბ</i> მ	169 GTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPT 220 
75 25 26	109 PLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLDPLQD 168        : :	ò 8	221 SVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEBEATSGLVMLCI 280 : :          : :                     : : 2638 -LTINTIASDDILNAAEAGSPLTISGTSTAE-TGQTVTVTL 2676
oy Dp	169 GTNTHIMATEASNYAQYRVARATIRYRPLUPNAUGGYAISISFWPQTTTTPT 220	& g	281 HGSLVNSYINTPYTGALGLLDFALELEFRNLTPGNINTRVSRYSSTARHR 330 : :
Qy Dp	221 SVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEBEATSGLVMLCI 280 : :	& 8	331 LRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLG 381 2728 LAVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEAGDVVSVVL 2776
Qy	281 HGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHR 330 : :	& a	382 GLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVV 439 2777
Qy Db	331 LRRCADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLG 381  2728 LAVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEXGDVVSVVL 2776	<b>상</b> 원	440 IQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTG 490
λ̈́o	382 GLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVV 439	λ	

	Db 2386 PFSSPGTATALPALRSTATTPTATSFTAIPSSSLGTTW-TRLSQTTTPWATMSTATPSST 2444  Qy 571 VENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTIDYPARAHT 622
RESULT 6 T4502b. tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-401-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Date: 21-401-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Date: 21-5025 R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A. J; Biol. Chem. 272, 3168-3178, 1997 A;Title: Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alternat A;Reference number: 222899; MUID:97166151; PMID:9018550 A;Accession: T45025 A;Accession: T45025 A;Accession: T45025 A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-3570 <des> A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503 A;Genetics: A;Genetics:</des>	RESULT 7 S52863 DNAbolinding protein R kappa B - human C;8pecies: Homo sapiens (man) C;8pecies: Homo sapiens (man) C;3pecies: Homo sapiens C;3pecies: A: Bouwmeester, T:; Scheidereit, C. R;Mieters A: Bouwmeester, T:; Scheidereit, C. Submitted to the EMBL Data Library, August 1994 A;Reference number: \$52863 A;Reference mRNA A;Reference: EMBL:X80878; NID:g695578; PID:g695579 A;Reidues: 1-1324 <nie> A;Reidues: 1-1324 <nie> A;Cross-references: EMBL:X80878; NID:g695578; PID:g695579 A;Cross-references: EMBL:X80878; NID:g695579 A;Cross-references: EMBL:X80878; NID:g695579 A;Title: Cloning of R kappa B, a novel DNA-binding protein that recognizes the interleuk A;Reference number: A45580; MUID:92135142; PMID:1777480 A;Accession: A45580 A;Accession: A45580</nie></nie>
Ouery Match  4.0%; Score 137; DB 2; Length 3570;  Best Local Similarity 20.1%; Pred. No. 6.7;  Matches 143; Conservative 72; Mismatches 257; Indels 240; Gaps 33;  Qy 52 AIPYIHPINPFAPDYIRAAGAGPRVROPARPIGSAMRDQAQRPAVASRRRFTTAGAAP 109  Db 1867 ALPALRSTATTPTATSVTAISSSIGTAWTRLSQTTPTAT 1907	A;Residues: 313-1292, ISNREQLIAPP', 1304, 'QSPLLL' <ada> A;Cross-references: GB:09191, GB:S79520, NID:9476273; PIDN:AAA17871.1; PID:9476274 A;Cross-references: GB:09191, GB:S79520, NID:9476273; PIDN:AAA17871.1; PID:9476274 A;NOte: sequence extracted from NCBI backbone (NCBIN:79520) C;Keywords: DNA binding; transcription factor C;Keywords: DNA binding; transcription factor Query Match 4.04; Score 135.5; DB 2; Length 1324; Best Local Similarity 19.0%; Pred No. 2;</ada>
110 LTAVAPAHDTPPVPDVDSRGALLRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDG 16	11Ve 95; MISMACCHES 232; INGGES 231; GAPS  ARPTGSAWRDQAQRPAVASRRPTTA 1  FINAL STATEMENT STATEME
Db 1947 TAHTTKVPTTTTTGFTAIPESSERGIALIFPVWISITITFIRGSIVI 1993  Qy 221SVDMNSITSIDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVML 278	Db 753 PALPAIDISPPPVSAVNKSGPSTVSEPAKSSSGVLLVSSPTMPHLG 798 QY 165PLQDGTNTHIMATEASNYAQYR-VARATIRYRPLVPNAVGGYAISI 209 Db 799 TMLSPASSQTAPSSQAAARVVSHSGSAGLSQVRVVAQPSLPAVPQQSGGPAQTLPQM 855
QY         279 CIHGSLVNSYTNTPYTGALGLLDFALELEF 308           Db         2044 AT-GSTINESSTEGTTPIPPVLTTTATTEATSSTVTP-SSALGTTHTPPVFNTTATTHG 2101           QY         309 RNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAAT	QY         210
Qy 348RPWKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLFTELISSAG 392  Db 2157 PHPSSRTTESPPSPGTTTPGHT-RGTSRTTATATPSKTRTSTLLPSSPTSAPITTVVTTG 2215  Qy 393 GQLPYSRPVVSANGEPTVKLYTSVENAQDKGI 425  i         :	300LDFALE 362 SIPLTATNFRIG 351 KDLYFTSTNGVG 1017
Qy 426AIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAP 458	411 KLYTSVENAQQDKGIAIPHD  : : :     ::    1068 KVTPDLKPTEASSSAFRLMPALGVSV 462 FSVLRANDVLWLSLTAAEYDO-   :     :     ::    110 AATTRIVQGLGVMPPRAGQTITVATHAKG 503 VATGAQAVARSLDW

	OY 388 ISSAGGOLFYSRPVVSANGEPTVKLYTSVENAQODKGIAIPH 429  1:
utinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c) ies: Xylella fastidiosa 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 mous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen 18-18-157, 2000 18-18-157, 2000 18-18-157, 2000 18-18-157, 2000 18-18-158-159 18-18-159 18-18-18-18-18-18-18-18-18-18-18-18-18-1	Oy 501 UNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKIFFVLPLRGKLSFWEAGTTKAGYPYN 560
A; Contented number: A59328 A; Contents annotation C; Genetics: A; Score 135.5; DB 2; Length 3282; Best Local Similarity 21.9%; Pred. No. 7.4; Matches 135; Conservative 64; Mismatches 216; Indels 201; Gaps 27; Oy 97 ASRREPTTAGAAPLMAVAPAHDTDDVD	as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V. E.; de Sa, R.G.; Santelli, R.V.; Sawasank, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaire
429 ASPADPTPVASVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHI 483  133 RRQYNLSTSPLTSSVATGTNLVLYAAPLSPL-LPLQDGTNTHIMATEASN 181  484 TAGGAIDAILTTLDNRDGTAALNRLTLQGQRLDNQHGILTLATEATHTHTHINN 537  182 YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIA 241  538 AAGQLHVNGTLDLTAQHLNNASGHLLTTGPQSATL-TIADLLDNTSGTLASA 588  242 SELVIPSERLHYRNQGWRSVETSGVAEEBATSGLVMLCIHGSLVNSYTNTPYTGALGLLD 301  589 GSLTITAATL	A: STRINGANO, M.H.; Valiada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; A; Reference number: A59328 A; Contents: annotation C; Genetics: A; Score 135.5; DB 2; Length 3442; Best Local Similarity 21.9%; Pred. No. 7.9; Matches 135; Conservative 64; Mismatches 216; Indels 201; Gaps 27; ASRRRPTAGAAPLTAVAPAHDTP
TDLSHA TAATRF   AALDNT	OY 182 YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIA 241

OY  133 RROYNLSTSPLTSSVATGTNLVLYAAPLSPL-LPLQDGTNTHIMATEASN 181  bb 484 TAGGAIDAILTTLDNRDGTAALNRLTLGGQRLDNGHGILLTLATEATIHTHTLNN 537  QY 182 YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIA 241  bb 538 AAGQLHVNGTLDLTAQHLNNASGHLLTTGPQSATL-TIADLLDNTSGTLASA 588  QY 242 SELLIYARDGWRSVETSGVAEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLD 301  CH 1		Db 740 TTGTWTNTGGHIOTTGPATLHATTLDNRGGILHTATGPLDLRITGTLNNQDNGLLTTT 797  430 D-IDLGESRVVIQDYDNQH-EQDRPTPSPAPSRPFSVLRANDVLML	OY 501 VNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYN 560	Nimitarisot, N.  Nimitarisot. 219425  A; Accession: T21460  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Status: DNA  A; Residues: 1-796 «WIL»  A; Cross-references: EMBL: 248582; PIDN: CAA88469.1; GSPDB: GN00020; CESP: ZK945.10  A; Experimental source: clone F27E5 C; Gene: CESP: ZK945.10  A; Gene: CESP: ZK945.10  A; Map position: 2  A; ILCONS: 62/3; 124/3; 169/1; 216/1; 262/3; 371/1; S81/3; 608/1  A; Introns: 62/3; 124/3; 169/1; 216/1; 262/3; 371/1; S81/3; 608/1  Noury Match  Best Local Similarity 20.6%; Pred. No. 1.4;  Matches 121; Conservative 61; Mismatches 228; Indels 176; Gaps 24;	APDVTAAAGGPRVRQPARPLGS   :
	Db 740 TTGTWINTGGHLQITGPATLHATTLDNRGGILHTATGPLDLRITGTLNNQDNGLLITT 797  Qy 430 D-IDLGESRVVIQDYDNOH-EQDRPTPSPAPSRPFSVLRANDVLWL473  Db 798 DALTLTAASLLNOHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRS 852  Qy 474 -SLTAABYDQSTYGSSTGPVYUSDSVTL 500        :	Qy 501 VNVATGAQAVARSIDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYN 560	RESULT 10 B82519 hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82519 C;Accession: B82519 C;Accession: B82519 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Note: Loomplete list of authors see reference number A59328 below A;Accession: B82519 A;Status: preliminary A;Accession: B82519 A;Status: Draliminary A;Residues: 1-3455 A;Cross-references: GB:AE003849; NID:g9108003; PIDN:AAF85560.1; GSPDB:GN001	A; Experimental source: strain 9a5c R; Simpson, A.J.G; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Brjones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.A.; Mathors: Martins, E.M.F.; Mathors: Martins, M.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Athoros: A.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.; Reference number: A59328 A; Contents: annotation C; Genetics: C;	A;Gene: XF27/5  Query Match Best Local Similarity 21.9%; Pred. No. 8;  Matches 135; Conservative 64; Mismatches 216; Indels 201; Gaps 27;  Qy 97 ASRRPTTAGAAPLTAVAPAHDTPPVPDVDSRGAIL 132  Cy

44410, ne prot MM> <cal></cal>		48 SPPRINTHTMPREPRUTAMAGAGENURGARP-LAGAMRDAGARRATH 105 705 SAPVANGSTYTSSPSAPVANSSTYTSSPSAPVANSSTYTSSPSAPALSSTY-18; 705 SAPVANGSTYTSSPSALVULSSTSTSPSAPVANSSTYTSSPSAPALSSTY-18; 706 GAAELTANDAADTPUPUCBRCALLERGYNLGYSSTYTSSPSAPALSSTY-18; 70 106 GAAELTANDAADTPUPUCBRCALLERGYNLGYSPST
	equence extracted from NCBI backbone (NCBIN:144410, NCBIP:144411) 3D:HKR1 eferences: SGD:SO002828; MIPS:YDR420w inton: 4R s: calcium binding; glycoprotein; transmembrane protein main: signal sequence #status predicted <sig> Froduct: HKR1 protein #status predicted <mat>  66/Domain: calcium binding #status predicted <im> calcium binding #status binding</im></im></im></im></im></im></im></im></im></im></im></im></im></im></im></im></im></im></im></mat></sig>	31023;

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probable membrane protein YJR151c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J2223; serine/threonine-rich protein YJR151c
C;Species: Saccharomyces cerevisiae
C;Accession: S57180
R;Scarcez, T.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57169
A;Reference number: S57169
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1161 <SCA>
A;Coss-references: EMBL:Z49651; NID:gl015902; PID:gl015903; GSPDB:GN00010; MIPS:YJR151c
C;Genetics:
A;Gene: SGD:DAN4; MIPS:YJR151c
A;Cross-references: SGD:S0003912
A;Map position: 10R
C;Keywords: transmembrane protein
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152 NLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISI-- 209
                            252 ILSITSSPVSSEAP--SATSSSVSSEASSTTSSSVSSEAPLATSSVVSSEAPSSTSSVVS 309
                                                                                                  368 VSSEAPSTISSSVSSEISSTKSSVMSSEVSSATSSLVSSEAPSAISSL--ASSRLFSSKN 425
                                                                                                                                                                                                                                                       426 TSVTSTLVATEASSVTSSLRPSSETLASNSIIESSLSTGYNSTVSTTSAASSTLGSKVS 485
                                                                                                                                                                                                                                                                                                         LTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP- 428
                                                                                                                                                                                                                                                                                                                                     486 SSNSRMATSKTSSTSSDL--SKSSVIFGNSSTVTTSPSASISLTAS-----PLPS 533
                                                                                                                                                                                                                                                                                                                                                                                 --HDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSITAAEYDQSTYG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIVSSITSSETTNESNLATSSTSLLSNKATARSLSTSNATSASNVPTGTFSSMSSHTSVI 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 YRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLT 312
                                                                                                                                                                                                                                                                                                                                                                                                                         534 VWSDITSSEASSISSNL-----ASSSAPSDNNSTIAS-----ASLIVIKTKNSVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 HPTNPFAPDVTAAAG------AGPRVRQPARPLGSAWRDQAQRPAVASRRR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 HKTETYPSEIAAAVFDYGDFTTRLTGISGDEVTRMI--TGVPWYSTRLKPAISSALSKDG
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                                                                            210 SFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 KPNMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSSSSAHPITLD 527
                                                                                                                                                            204 G-YAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIAS---ELVIPSERLHYRNQGWR 259
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                                                                                                                                                                                                                                                                                                                 VSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTL 379
                                                                                                                                                                                                                                                                                                                                                                                           380 LGGLPTELISSAGGQLFYSRP-----VVSANGEPTVKLYTSVE-NAQQDKGIAIPHD 430
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                                                                                                                    88 VITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIESTTTVGPHASSSVA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein YM924.09
CiSpecies: Saccharomyces cerevisiae
CiSpecies: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
                                  SVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                                                                                                                                                                                                                                                                 240 VDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLA------AQTT
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Best Local Similarity 18.7%; Pred. No. 3.2;
Matches 113; Conservative 109; Mismatches 262;
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R;Churcher, C.M.
submitted to the EMBL Data Li
A;Reference number: 559302
A;Accession: 559310
A;Accession: 4599010
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R RT S	Fry "Hep full Viro	K.E., F patitis  -length plogy 18	Fry K.E., Reyes G.R.; "Hepatitis E virus (HEV): mc full-length viral genome."; Virology 185:120-131(1991):- FUNCTION: CONTAINS A HIC	R.; (HEV): mo genome."; 31(1991).	: 1 : 1 HI(	molecular ; iGH BASIC	lar cloning SIC AMINO AG	r and sequencing	·d 00	the ING	
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Virus Genes 7:95-109(1993).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
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Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata
Rikihisa T., Winn K.;
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TSATEV S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,

Malik I.A., Igbal M., Purcell R.H., Edge strain of hepatitis E virus.";

Transacterization of a prototype strain of hepatitis E virus.";

Proc. Natl. Acad. Sci. U.S.A. 89:559-563 (1992).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING

THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA

BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORP2).
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; SERNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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IIIterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA
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                                                                                                                                                                                                                                                                                                                              560 STRUCTURAL PROTEIN 2.
70998 MW; 3A82A4EA255C6253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                       Score 3367; DB 1;
Pred. No. 8.8e-206;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                        InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
Signal.
1 22 BY SIMI
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98.9%;
                                                                                                                                                                                                     EMBL; D10330; BAA01174.1; -.
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Best Local Similarity 98.9
Matches 653; Conservative
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660
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                                                                                                                                                                                                                                                                                                           "Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                E virus (HEV).";
Virology 191:550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Indels
                                                                                                                                                                                                                                                             J., Yun K.Y., Fry K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 BY SIMILARITY.
659 STRUCTURAL PROTEIN 2.
70640 MW; CF75E75EFD8FBE2C CRC64;
                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA Hepatitis E-like viruses.
01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.0%; Pred. No.
                                                   Structural protein 2 precursor.
Hepatitis E virus (strain Mexico) (HEV)
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PIR; B44212; B44212.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                       Huang C.C., Nguyen D., Fernandez J.
Bradley D.W., Tam A.W., Reyes G.R.;
                                                                                                                                                                                                                                     MEDLINE=93079857; PubMed=1448913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF03014; SP2; 1. Signal.
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659 AA;
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Matches 614; Conserv
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=31768;
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VST2 HEVME STANDARD; Q03550; 01-OCT-1993 (Rel. 27, Created)

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                                                                                                                                                               TKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLED 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G1.";
Mol. Cell. Biol. 16:3264-3274(1996).
PUNCTION: Seems to be involved in the correct timing of cell
separation after cytokinesis, as separation of mutant daughter
cells is delayed. Could either be an enzyme necessary for glucans-
degradation of the cell wall at the neck region between mother and
daughter cells or a requiatory protein controlling this metabolic
step. Exclusively expressed between the end of mitosis and early
G1; inactivated before cells pass start.
         LGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTGPV
                                 YVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGT
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EMBL; 246259; CAA86371.1; -.

EMBL; 271603; CAA96259.1; -.

FRBL; 558662; 558662.

GermColline; 14333; -.

SGD; S0005271; EGT2.

SGD; GO:0009277; C:cell wall (sensu Fungi); IDA.

GO; GO:000917; C:cell wall (sensu Fungi); IDA.

GO; GO:000910; P:cytokinesis; IMP.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95373280; PubMed-7645347; Maftenin C.; Matenin W., Nicaud U.-M., Levesque H., Gaillardin C.; Mattening analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PAS8 and KREI loci, five new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kovacech B., Nasmyth K., Schuster T.,
"EGT2 gene transcription is induced predominantly by Swi5 in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeas).
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Sacchascharomycetales; Saccharomycetales; Saccharomycetales, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SEQUENCE FROM N.A.
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                   480 DQSTYGSSTGPVYISDSVTLVNVATGAQAVĀRSLDWSKVTLDGRPLPTVEQYSKTFFVLP
                                                                                                   DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLST1QQYSKTFFVLP
                                                                           LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                     LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
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M., Rikihisa T., Mizuno
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                                                                                                                                                                                                                                                                                                                                                                         Structural protein 2 (Fragment).
Structural protein 2 (Fragment).
Viruses, ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=31766;
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Pred. No. 1.2e-147;
1; Mismatches 4;
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                           485 AA.
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Wang C.-K., Shikata T., Ichikawa M.,
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InterPro; 1PR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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99.0%;
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ID _VST2_HEVRH
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REAL MEDLINE-21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barril W.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Blard C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Gleggan J.C., Clamp M., Clark R.E., Cornor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Cornor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Cornor R.E., Corby N.R.,
Clulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Grafham D.V., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Ay M.P., Kinberley A.M., King A., Khights A., Laird G.K., Lawlor S.,
RAY M.P., Martin S.L., McConnachie L.J., McLay K., Mchurray A.A.,
RAY M.P., Mint S.L., McConnachie L.J., McLay K., Mchurray A.A.,
RAY M.P., Mistry D., Moore M.J.F., Mullkin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Bentley D.R., Williams L., RA William P. M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                              900
728 TE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMVSSTKLTEATATDKGDAYSVIS 783
                                                                                                                  844 VIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIKGSKTSLSTEESVVAGYSTTVG
                                -OYSKTFFVLPLRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97336072; PubMed=9192867;
Mengus G., May M., Carre L., Chambon P., Davidson I.;
"Human TAF(II) 35 potentiates transcriptional activation by the AF-2s
of the retinoic acid, vitamin D3, and thyroid hormone receptors in
mammalian cells.";
                                                               784 STQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTCTESGQATEYGSLIPISTLDGS
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                                                                                                                                                                                                                                                                          T2D3 HUMAN STANDARD, PRT; 1083 AA.
000268; 099721; 09BR40; 09BR42;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence relation update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2010 (Rel. 43, Last annotation update)
17-WAR-1010 (Rel. 13) (APFII-136)
17AFII135) (TAFII-130)
TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAFII135 OR TAFIII30.
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                               545 LSFWEAG-----TTKAGYPYNYNTTASDQLLVENAAGHRVAIST
                                                                                                                                                                                           901 AAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDSAQYAEHT
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                                SLDWTKVTLDGR -- PLSTIQ-
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                                                                 Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; TAS
                                                                                                                                                                                                                                                  pairs.";
Mol. Cell. Biol. 20:340-351(2000).
Mol. Cell. Biol. 20:340-351(2000).
PUNCTION: Makes part of TFIID is a multimeric protein complex that plays a central role in mediating promoter responses to various activators and repressors. Potentiates transcriptional activation by the AF-2S of the retinoic acid, vitamin D3 and thyroid hormone... SUBUNIT: TFIID is composed of TATA binding protein (TBP) and a number of TBP-ascociated factors (TAFE). Component of the TFTC-HAT complex, at least composed of TAFEJ. TAFEJ, SUBDAIL, SUPTSH/SPT3, TAFEZ/TAFIISO, TAFEZ/TAFIISO, TAFEZ/TAFIIOO, GCNSIZ/GCNS, TAFIO
                                                                                                                                                                                                                        "The human TFIID components TAF(II)135 and TAF(II)20 and the yeast SAGA components ADA1 and TAF(II)68 heterodimerize to form histone-like
                                                                                    complex
                                                                                                                                                                                MEDLINE=20063193; PubMed=10594036;
Gangloff Y.-G., Werten S., Romier C., Carre L., Poch O., Moras D.,
Davidson I.;
                           DENTIFICATION IN THE TFTC-HAT COMPLEX WITH TAF5L; TAF6L; TADA3L;
                                                                                                                                                      OF 870-918 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIN, 601796; -. GO, Ctranscription factor TFIID complex; TAS. GO; GO:0016515; F:general RNA polymerase II transcription fac. GO; GO:0016515; F:general RNA polymerase II transcription fac. GO; GO:0003713; F:transcription co-activator activity; TAS. InterPro; IPR007900; TAF4.
                                        SUPT3H; TAF2; TAF5; TRRAP; GCN5L2 AND TAF10.
MEDLINE=99303588; PubMed=10373431;
Brand M., Yamamoto K., Staub A., Tora L.;
"Identification of TATA-binding protein-free TAFII-containing subbunits suggests a role in nucleosome acetylation and signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPPSPRRPLVPA -> GRGLLQQRGGRES
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 Natl. Acad. Sci. U.S.A. 93:13611-13616(1996)
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G -> GPG (IN REF. 2).

MISSING (IN REF. 3).
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                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                   transduction.";
J. Biol. Chem. 274:18285-18289(1999).
[5]
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SMART; SM00549; TAFH; 1.
Transcription regulation; Nuclear
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EMBL; AL137077; CAC36006.1; -.
EMBL; AL109911; CAC22112.2; -.
EMBL; U73308; AAC50901.1; -.
PDB; 1H30; 26-SEP-02.
TRANSPAC; T02328; -.
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                                                                                                                                                                                                                                                                                                                                                                             ----PTTAGAAPLTAVAPAHDTPPVPDVDS---RGAILRRQYNLSTSPLTSSVATGTNL 153
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Chen Y., Di Y.P., Wu R.;
"Molecular cloning of the amino-terminal and 5'-flanking region of the
human MUGSB mucin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                          PMLPAP-----PPGQPSG------RRRGRRSGGS------GGGFWGDRVDSQP
                                                                                                                                                                                                                                                                          51 FAIPYIHPINPFAPDVTAAAGA-GPRVROPARPLGSAWRDOAQRPAVASRRR-----
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q9HC84, 000447; 000573; 014985; 015494; 095291; 095451; Q14881;
Q99552; Q9UE28;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Mucin 5B precursor (Mucin 5 subtype B, tracheobronchial) (High molecular weight salivary mucin Mol) (Sublingual gland mucin).
                                                                                                                          177;
                                                                           Length 1083;
                                                                                                                             Indels
293 293 P -> L (IN REF. 3).
1083 AA; 109943 MW; A6453827572A0752 CRC64;
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                                                                           DB 1;
                                                                                                ilarity 21.1%; Pred. No. 0.5;
Conservative 65; Mismatches 241;
                                                                         4.0%; Score 137.5;
21.1%; Pred. No. 0.5
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(See http://www.isb-sib.ch/announce/
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InterPro; IPR006208; Cys knot.
InterPro; IPR006208; Cys knot.
InterPro; IPR006209; Cys knot.
InterPro; IPR009041; PMP_inhibitor.
InterPro; IPR001919; TIL_Cysrich.
InterPro; IPR00107; VWF_C.
InterPro; IPR001065; VWF_C.
InterPro; IPR0010846; VWF_D.
Pfam; PF00003; VWc; 1.
Pfam; PF00003; VWc; 1.
Pfam; PF00003; VWc; 1.
Pfam; PF000181; VWc; 6.
SMART; SW00216; VWD; 4.
SMART; SW00216; VWPC_1; 2.
PROSITE; PS01128; CTCK 1; 1.
PROSITE; PS01128; CTCK 2; 1.
PROSITE; PS01128; CTCK 2; 2.
Glycoprotein; Repeat; Signal, Polymorphism SIGNAL
      entities requires a license agreement (or send an email to license@isb-sib.ch)
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EMBL; X74955; CAA52910.1; -...
EMBL; UG3836; AAB61398.1; -...
EMBL; U78554; AAC51344.1; -...
EMBL; U78552; AAC51344.1; -...
EMBL; U78553; AAC51344.1; -...
EMBL; U78551; AAC51343.1; -...
EMBL; U95031; AAC51343.1; -...
EMBL; Y09788; CAA70926.1; -...
Genew; HGNC:7516; MUC5B.
                                                                  AF086604; AAC67545.1; -. AJ004862; CAA06167.1; -.
                                                    EMBL; AF107890; AAG33673.1; -.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
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Desseyn J.-L., Buisine M.P., Porchet N., Aubert J.-P., Laine A.;
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MEDLINE-96125355; PubMed-8554565;
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                                                                                                                                                                                                                                                                   TISSUB=Placenta;
MEDLINE=97166151; PubMed=9013550;
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                                                                                                             Biochem. Biophys. Res. Commun. 251:350-355(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=97347489; PubMed=9201995;
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Salivary gland;
MEDLINE=97292540; PubMed=9147051
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3600 LGQVVECSLDFGLVCRNREQVGKFKMCFNYEIRVFCCNYG--HCPSTPATSSTATPSSTP 3657
                                                                                                                       GTTWILTK-----LTTTATTTESTGSTATPSSTQGPPAGTPHVSTTATTPTV-TSSKAT 3710
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WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
Weod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squoros U., Peat N., Hayles J., Basham D., Bowaman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Ra Brooks K., Gonnor R., Cronin A., Davis P., Feltwell T., Fraser A., Gonlins M., Connor R., Cinllingworth T., Churcher C.M., Ra Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holrody S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Ra Mooney P., Woule S., Murphy L., Niblett D., Odell C., R. Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Rutherford K., Simmonds M., Squares R., Squares S., Stevens K., Stevens K., Stevens K., Andley R., Walther S., Warren T., Whitehead S., Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woltjens I., Beck A., Walsh S.V., Warren T., Whitehead S., Rottiens I., Langer I., Beck A., Lehrach H., Reinhardt R., Purnelle B., Beger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Andeler E., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Langa R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Lowa M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Lander S., Armstrong J., Forsburg S.L., Rabadovski G.V., Ussery D., Barrell B.G., Nurse P.; RT Mediner B. Schlassacharomyces pombe."; R. Matter B. St., Matter B. 
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                                                                      SRPFSVLRANDVLWLSLTAAEXD-----QSTYGSSTGPVYVSDSVTLVNVATGAQAV 510
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28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical serine/threonine-rich protein C19G12.16c in chromosome
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Schizosaccharomyces pombe (Fission yeast).
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                            CARBOHYD
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MEDLINE=94156857; PubMed=8113191;
Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
Yabe T., Nakajima T., Ichishima E., Furnichi Y.;
"Cloning of the Saccharomyces cerevisiae gene whose overexpression overcomes the effects of HM-1 killer toxin, which inhibits
beta-glucan synthesis.";
                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Hansenula MRAKII killer toxin-resistant protein 1 precursor.
                                                                                                                 SEQUENCE FROM N.A.
                                                    HKR1 OR YDR420W.
                                                                                            NCBI_TaxID=4932;
                                                                                                                            STRAIN-YNN 295;
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                                                                                                                                                                                                                                                                                                                                                                                                        VSSSSLSSFT-PSYSTNLTTTG--STTTTGSATVSSSPFYSNSSVIPTSVPSS-VSSFTS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                    -NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATR 348
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                            HYPOTHETICAL SERINE/THREONINE-RICH PROTEIN C19G12.16C.
                                                                                                                                                                                                                                                                       20.5%; Pred, No. U.5;
tive 77; Mismatches 235; Indels 160;
                                                                                                                                              POTENTIAL)
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                                                                                                                                                                                                                                           68E8D1CFB855F8A8 CRC64;
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                                               SER/THR-RICH.

N-LINKED (GLCNAC.

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                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                  (GLCNAC
           Signal.
                                                                                                                                                                                                                                                               Score 133;
Pred. No. 0
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N-LINKED
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      Hypothetical protein; Glycoprotein; SIGNAL 1 19 DOWNERS
SPombe; SPAC19G12.16c;
                                                                                                                                                                                                                                           68262 MW;
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                                                                                513
670 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    J. Bacteriol. 176:1488-1499(1994).
    -!- FUNCTION: Could regulate beta-glucan synthesis. Overexpression provides resistance to Hm-1 killer toxin.
    -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
    -!- PTM: Could be O-glycosylated in the serine/threonine-rich domain.
    -!- SIMILARITY: SOME, TO YEAST MSB2.

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12 X 28 AA TANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-A-P-A-A-I-S-S-T-
Y-T-S-S-P.
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HANSENULA MRAKII KILLER TOXIN-RESISTANT
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19.0%; Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                         Repeat; Signal.
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1802 AA

PRT;

STANDARD;

HKR1\_YEAST ID HKR1\_YEAST

RESULT 10

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61; Mismatches 228; Indels
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GLY/SER-RICH
                                                                                                                                                    InterPro; IRR00211; Cat_channel_TrpL.
InterPro; IRR00211; Cat_channel_TrpL.
InterPro; IRR00111; Cat_chans.
InterPro; IRR001024; Lipxygenase_LH2.
InterPro; IRR0001024; Lipxygenase_LH2.
InterPro; IRR000203; PKD_Cys_rich.
InterPro; IRR0008976; PLAT_LH2.
Flam; PRO1825; GPS; I.
Pfam; PRO1825; GPS; I.
Pfam; PRO1437; PLAT; 1.
PRINTS; PRO1437; PLAT; 1.
SMART; SM00303; GPS; I.
SMART; SM00308; LH2; I.
                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%; Score 133;
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EMBL; Z48582; CAB70192.1; JOINED.
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Hypothetical protein; Tr
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     GAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLP 165
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Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 1 GPS domain.
-!- SIMILARITY: Contains 1 PLAT domain.
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                                                            LQDGTNTHIMATEASNY------AQYRVARATIRYRPLVPNAV---
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01-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
Hypothetical protein ZK945.9 in chromosome II.
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Caenorhabditis elegans.
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Wilkinson-Sproat J.;
Submitted (FEB-1995)
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TFYDSTSVNLTLNSGLGIIGYQTSIECTSPTSSNYVSTTKDGACFTKSVSMPRLGGTYPA
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                                                                                                   QH-EQDRPT-----PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVS---
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                                                                                                                                                                                                                                                                                                                                                                          Hypothetical 138.1 kDa protein in FLO9-GDH3 intergenic precursor
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288c / AB972;
MEDLINE=95249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C
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-!- SIMILARITY: STRONG, TO YEAST PROTEIN FLOI.
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SGD; S0000059; YAL0637C.
InterPro; IPR001389; Flocculin.
Pfam; PF00624; Flocculin; 13.
Hypothetical protein; Glycoprore SIGNAL.
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Hall J., Ouel
Storms R.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036 SISSA----IVSTATVTVSGATTE--YTTWCPISTTEITKQTTETTKQTKG-TTEQTTET 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .089 TKQTTVVTISSCESDVCSKTASPAIVSTSTATINGVTTEYTTWCPISTTESKQQTTLVTV 1148
                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                           643 WNDTFTSTSTEMITVTGTNGLPTDETIIVIRTPTTATTAMTTTQPWNDTFTSTSTEITTV 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISSAGGQLFYSRPVVSANGEPTVKLYT-----SVENAQQDKGIAIPHDIDL 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFISSPVISSTITSASILS---ESSKSSVIPTSSSTSGSSESET-----GSASSASS 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                           --TPTSEGLVTTTTEPWTGTFTS-TSTEMTTITGTNGQPTDETVIIVKTPTTAISSSLSS
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                                                                                                                                                                                                                                                                                                                                                                                                      -----VASRRRPTTAGAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD-----VRILVQP--GIASELVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----bvvtvystwrpotineo----
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glucoamylase S2 precursor (BC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGVPTDETVIVIRTPTSEGLISTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIR--
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 GESRVVIQDYDNQHEQDRPTPSPA----PSRPFSVLRANDVLWLSLTAAEYDQST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBL_TaxID=41870;
                                                                                                                                                                                                                                                            WGDRVDSQPFAIPYIHPTNPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPA-
овь вив N-LINKED (GLCNAC. . .) (POTENTIAL)
1322 AA; 138072 MW; AADFDIFF13267CEA CRC64;
                                                                                                                                                                              Indels 166;
                                                                                                                                                                                      92; Mismatches 289;
                                                                                                               1;
                                                                                                                   DB
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                                                                                                           Score 131;
Pred. No. 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                   284 LVNSYT---NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE 340
                                                                                                                                                                                                                                                                                                                                                                                   LITIAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TTTVVTTESST-----GTNSAGK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTSYTTKSVPTTY-----VFDFGKG1-----LDQSCGG----VFSNNGSSQVQLRD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VENAQQDKGIAIPHDID-LGESRVVIQDYDNQHEQD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PSILPGVVIASPSOTHPDYFYOWIRDSALTINSIVSHSADPAIETLLQYLNVSFHLQRT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVLMNG--TV-VYDSNGAWDSSPLEEWLQRQKKVVSIERIFENIGPSAVY-----364
TITTTVCSTGINSAGETTSGCSPKIITTTVPCSTSPSETASESITTSPTTPVTVVSTTV
                                                                                                             SFWPOT-TTTPTSVD
                                                                                                                                                                                224 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                                                                                                                                                                                                                                ----TSGCSPKTVTT--TVPCSTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21113168; PubMed=11160904; Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry C.V.; "Induction and repression of DAN1 and the family of anaerobic mannoprotein genes in Saccharomyces cerevisiae occurs through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wall (By similarity)
to the membrane by a (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FSVLRANDVLWLSLTAA-
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    -!- PTM: Extensively O-glycosylated (Potential).
    -!- SIMILARITY: Belongs to the SRP1 / TIP1 family.

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01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cell wall protein DAN4 precursor.
DAN4 OR YURISIC OR J2223.
                                                                             MATEASNYAQYRVARATIRYRPLVPNAVGGYAISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1161 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex array of regulatory sites."
Nucleic Acids Res. 29:799-808(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 RGKLSFWEAGTTKAGYPYNYTTA
                                                                                                                                                                                                                                                                                                                                      --GEYTTEATAPVTTAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 RPT-----PSPAPSRP-
                                                                                                                                                                                                                                   TNSAGET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scarcez T.;
Submitted (SEP-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAN4 YEAST
P47179;
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                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 PPVPDVDSRGAILRRQYNLSTSP--LTSSVATGTN---LVLYAAPLSPLLPLQDGTNTHI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                                                                                                                                                           chains
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INTERACT WITH SUBSTRATES (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                   s of terminal 1,4-linked alpha-D-from non-reducing ends of the ch
                                                                                                                                                     MEDLINE=91276266; PubMed=2055484;
indrocehts M.G., Precorius I.S., Sollitti P., Marmur J.;
"Primary structure and regulation of a glucoamylase-encoding gene
(STA2) in Saccharomyces diastaticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000165; Glyco hydro_15.
InterPro; IPR008928; Glyco_trans_6hp.
Pfam; PR00723; Glyco hydro. 15; 1.
PRINTS; PR00736; GLHYDRLASE15.
PROSTITE; PS00820; GLHOOMYLASE; 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
Kim K., Bajszar G., Lee S.Y., Knudsen F., Mattoon J.R.; "Cloning of a new allelic variant of a Saccharomyces diastaticus glucoamylase gene and its introduction into industrial yeasts."; Appl. Biochem. Biocheml 44:161-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 193;
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Y SUBUNIT.
SUBSTRATE (BY SIMILARITY).
CATALYTIC BASE (BY SIMILARITY)
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3FAC172C128AOC6F CRC64;
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); Mismatches 231;
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(GLCNAC.
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                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Hydrolysis of terminal glucose residues successively from non-redu with release of beta-D-glucose.
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                                EMBL; Z49021, CLOSTING, S57180; S60109327; C.CEIL wall (sensu Fungi); IDA.
InterPro; IPR000992; SRP1 TIP1.
PROSITE; PS00724; SFP1 TIP1.
PROSITE; PS00724; SFP1 TIP1.
Cell wall; G1ycoprotein; Membrane; GPI-anchor; Signal; Lipoprotein.
Coll wall; G1ycoprotein; Membrane; Membrane; Signal; Lipoprotein.
                                                                                                                                                                                CELL WALL PROTEIN DAN4.
REMOVED IN MATURE FORM (POTENTIAL)
                                                                                                                                                                                                                                                                                                     95; Mismatches 274; Indels 133;
                                                                                                                                                                                                                                                                       Score 130.5; DB 1; Length 1161;
                                                                                                                                                                                                             GPI-anchor amidated asparagine
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
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send an email to license@isb-sib.ch)
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Similarity 17.2%;
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                             EMBL; Z49651; CAA89684.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM
                                                                                                                                                                                                                                                                      SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of an ~1 Mb region containing the MEF2B gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
10-OCT-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan
CSPG3 OR NCAN OR NEUR.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G., "Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00181; EGF_Ca.
InterPro; IPR001801; EGF_Tike.
InterPro; IPR001100; Ig-Tike.
InterPro; IPR0013599; Ig.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
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InterPro; IPR000152; Asx hydroxyl_S.
Thenno742; EGF_2.
                                                                                                                                                                              MEDLINE=99013874; PubMed=9795216;
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SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; IINK; 2.
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ProDom; PD000918; Link; 2.
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Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
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Pfam, PF00047; ig; 1.
                                                               (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---HDTPPVPDVD-SRGAILR-RQYNLSTSPLTSSVATGTNLVLYAAPLS-----PLLPL 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         763
                                              PGQPSGRRRGRRSGGSGGGF-----WGDRVDSQP----FAIPYIHPTNPFAPDVT
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22.0%; Pred. No. 2.1;
tive 63; Mismatches 231; Indels 201; Gaps
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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/FTId=VAR 016176.

N -> Y (IN REF. 2).

G -> R (IN REF. 2).

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  ASX HYDROXYL; 1.
C TYPE LECTIN 1; 1.
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Matches 140; Conservative
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PROSITE; PS00010; A: PROSITE; PS00615; C PROSITE; PS00615; C PROSITE; PS01186; E PROSITE; PS01186; E PROSITE; PS01187; E PROSITE; PS0124; E PROSITE; PS01241; L
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MEDLIN=-20271579; PubMed=10813471;
MEDLIN=-20271579; PubMed=10813471;
MEDLIN=-20271579; PubMed=10813471;
MEDLIN=-20271579; PubMed=108147;
Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
"Phylogenetically distinct hepatitis E viruses in Pakistan.";
EMBL; API85822; AAG16766.1;
"GO: 00005198; F:structural molecule activity; IEA.
InterPro; IPRO04261; SP2.
InterPro; IPRO04561; SP2.
InterPro; IPRO04561; Viral_cap_coat.
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SEOUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;
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Pred. No. 1.2e-213;
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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  Matches 657; Conservative
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                                                                             2004, 13:24:37; Search time 42 Seconds (without alignments) 4958.143 Million cell updates/sec
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O91855 hepatitis
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. 4.6e-213;
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MEDLINE=99350000; PubMed=10423137;
Arankalle V.A., Paranjape S., Emerson S.U.,
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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J. Gen. Virol. 80:1691-1700(1999).
BMBL; AF124407; AAD45493.1;
CO, GO:0005198; F:structural molecule InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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MEDLINE=99105430; PubMed=9880424;

TSarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;

"Phylogenetic analysis of hepatitis E virus isolates from Egypt."

"Med. Virol. 57:68-74[1999).

EMBL; AF051351; AAC35761.1;

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR004261; SP2.

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Hepatitis E-like viruses.
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 Pfam; PF03014; SP2;
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MEDLINE=95176571; PubMed=7871758;
Yin S., Purcell R.H., Emerson S.U.;
"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
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the EMBL/GenBank/DDBJ databases
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Hepatitis E-like viruses.
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EMBL; L25547; AAA31080.1; -.

EMBL; L25555; AAA51080.1; -.

GO; GO:0005198; F:structural molecule
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Yin S.R., Purcell R.H.,
Submitted (MAR-1996) to
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SEQUENCE FROM N.A.
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                                                    Score 3382; DB 12;
Pred. No. 5.3e-213;
1; Mismatches 5;
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SEQUENCE FROM N.A.
MEDLINE=92024067, PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Fry K.E., Reyes G.R.; Whepatitis E virus (HEV): molecular cloning and full-length viral genome.";
Virology 185:120-131(1991).
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301 DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360
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"Identification of the 5' Capped and 3' Complete Terminal Sequence it the Hepatitis E virus Isolated From Morocco.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY230202; AA072992.1; -..
GO; GO:0005198; F:structural molecule activity; IEA.
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MEDLINE=99107414; PubMed=9892396;
MEDG J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
Khudyakov Y.E.;
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SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;
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Hepatitis E-like viruses.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein 2 (Structural viral protein).
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InterPro; IPR008975; Viral_cap_coat.
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J. Med. Virol. 57:126-133(1999)
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                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of a hepatitis E virus isolated from the Xinjiang epidemic (1986-1988) of China."; Nucleic Acids Res. 20:3512-3512(1992),
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MEDLINE-93348763; PubMed-8346669;
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Virus Res. 28:233-247(1993).
GO: GO:0005198; Fstructural molecule activity; IEA.
InterPro; IPRO0426; SP2.
InterPro; IPRO08975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92115700; PubMed=1731327;
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SEQUENCE FROM N.A.
MEDLINE=92335008; PubMed=1630924;
Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T., Zhuang H.,
Win K.M.;
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SEQUENCE FROM N.A.
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Uchida T.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; D11033; BAA01867.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence.
Hepatitis E virus.
Viruses; seRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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98.6%; Pred. No. 2.4e-212;
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von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X99441; CAA67804.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ORF1, ORF2 & ORF3.
Hepatitis E virus.
Hepatitis E seRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Pred. No. 1.8e-212;
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                                                             PVPDVDSRCAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
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"Sequence analysis of full length HEV clones derived directly human liver in fulminant hepatitis E.";
(In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
VIRAL HERATITIS AND LIVER DISEASE, pp.313-316,
Edizioni Minerva Medica, Torino (1997).
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EMBL; X98292; CAA66937.1; -.
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Hepatitis E virus.
Hepatitis E senA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=12461;
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GO; GO:0005198; F:structural molecule
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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01-OCT-2003 (TrEMBLrel.
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MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis B virus isolates from Egypt."
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Pred. No. 5.1e-212;
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Hepatitis E virus.
Viruses; SSRNA positive-strand viruses, no l
Hepatitis E-like viruses.
NCBI_TaxID=12461;
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MEDLINE=22072932; PubMed=12076829;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
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                                                                                                       98.7%; Score 3362; DB 12;
98.8%; Pred. No. 1.1e-211;
iive 0; Mismatches 8;
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Submitted (MAR-1990) to the EMBL/GenBa
EMBL; AF051830; AAC97188.1; -.
EMC GO:00005198; Estructural molecule
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
SEQUENCE 660 AA; 70799 MW; A04C018
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MEDLINE=99049628; PubMed=9833882;
Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
"Hepatitis E virus: complete genome sequence and phylogenetic
    999
  Length
                           Indels
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OSMILLA:
O1-NOV-1999 (TrEMBIrel. 12, Created)
O1-NOV-1999 (TrEMBIrel. 12, Last sequence update)
O1-OCT--2003 (TrEMBIrel. 25, Last annotation update)
Capsid protein.
Hepatitis E virus.
Hepatitis E like viruses; ssRMA positive-strand viruses; no DNA stage;
Hepatitis E-like viruses.
 Score 3367; DB 12;
Pred. No. 5.1e-212;
4; Mismatches 6;
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Virus Res. 57:21-26(1998)
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Matches 650; Conservative
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                                                                                                                                     "An Indian strain of hepatitis E virus (HEV): cloning, sequence, expression of structural region and antibody responses in sera findividuals from an area of high-level HEV endemicity.";
                                                                                                        M., Ansari I.H., Ozdener M.H.,
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Ansari I.H., Nanda S.K., Durgapal H., Jameel S., Panda S.
Ansari I.H., Nanda S.K., Durgapal H., Jameel S.,
Translational analysis of complete HEV genome.";
Submitted (Jul.-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, U22532, AAA97366 1;
EMBL, AF076239; AAA77365 1;
GQ, GQ0019198; F. SETRUCTURAL molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03014; SP2; 1. _ _ SEQUENCE 660 AA; 70936 MW; 948556F804382EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      97.9%; Score 3336; DB 12;
ilarity 98.0%; Pred. No. 5.5e-210;
Conservative 3; Mismatches 10;
                                                                        STRAIN=HYDERABAD;
MEDLINE=96087204; PubMed=8567900;
Panda S.K., Nanda S.K., Zafrullah
Hepatitis E-like viruses
NCBL_TaxID=12461;
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Best Local Similarity
Matches 647; Conserva
                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                    1; Gaps
     hepatitis E virus based of following long RT-PCR.";
                                                                                                                                                                                                                                                 629;
                                                                                                                                                                                                                                            98.1%; Score 3342.5; DB 12; Length 98.3%; Pred. No. 2e-210; ive 1; Mismatches 9; Indels
                                                                  SEQUENCE FROM N.A.
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
ENBL; AF459438; AAM66330.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PP03014; SP2; 1.
SEQUENCE 659 AA; 70842 MW; ABCC177EBE6012C8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0RF-2.
Hepatitis E virus.
Viruses; sSRNA positive-strand viruses, no DNA stage;
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"Reevaluation of a North India isolate of
the full-length genomic sequence obtained
Virus Res. 86:53-58(2002).
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Matches 649; Conservative
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Best Local
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61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                                      AZACHANIA SADVINIA SADY
RX MEDLINE-21996248; PubMed=12001054;
RX TRAIN=JUN-SADY
RA TAKABASH K., Kang J.-H., Ohnishi S., Hino K., Mishiro S.;
RA Takabash K., Kang J.-H., Ohnishi S., Hino K., Mishiro S.;
RT Genetic Heterogeneity of Hepatitis E Virus Recovered from Japanese
RT Patients with Acute Sporadic Hepatitis.";
RJ J. Infect. Dis. 198:1342-1345 (2002).
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR HOEFPRO; IPRO08975; Viral_cap_coat.
DR InterPro; IPRO08975; Viral_cap_coat.
DR Pfam; PF03014; SP2; I.
SQUENCE 660 AA; 70980 MW; 19233C22F3E57FF8 CRC64;
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                                                                           LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA stage;
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Last annotation update)
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92.1%; Pred. No. 1.6e-199;
tive 26; Mismatches 26;
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Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                          Created)
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Matches 607; Conservative
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                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis E virus.
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Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                ORF2 protein.
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J. Infect. Dis. 185:134-215.

EMBL, AB074915; BAB96557.1; -.

GO, GO:005198; F:structural molecule activity; IEA.

Interpro, IPR004261; SP2.

Pfam, PR03014; SP2, 1.

SEQUENCE 674 AA; 72591 MW; 5C196112F81A2265 CRC64;
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                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                              Viruses, ssRNA positive-strand viruses,
Hepatitis E-like viruses.
NCBI_TaxID=12461;
                                                                                                                          Created)
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MEDLINE=21996248; PubMed=12001054;
                                                                                                                                                                                                                                                                                                                                                                                                   Mishiro S.;
Submitted (NOV-2001) to the
                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
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es 607; Conservative
                                                                      PRELIMINARY;
                                                                                                                                                                                                                           Hepatitis E virus.
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SEQUENCE FROM N.A.
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Sequence 15, Appl
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Sequence 10, Appl
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Sequence 2, Appl
                                                                                       August 16, 2004, 13:33:52; Search time 19 Seconds (without alignments) 1793.323 Million cell updates/sec
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/cgm2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-25-148A-19
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US-08-448-054-13
US-08-542-638-13
US-09-553-427-8
US-09-553-427-8
US-09-553-427-8
US-09-462-606-50
US-09-462-606-12
US-08-840-316-2
US-08-862-606-53
US-09-462-606-53
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US-08-542-634-14 PCT-US55-13703-14 US-09-462-666-48 SS-03-09-462-666-48 SS-03-09-168-16 US-08-259-148A-20 US-08-481-054-20 US-08-481-420 US-07-876-941A-20 US-08-477-292-14 US-09-172-699-16 US-09-172-699-16 US-09-172-699-16 US-09-172-699-16 US-08-477-292-15 SS-08-542-634-15 SS-08-542-634-25	ALIGNMENTS  US/08240049B  US/08240049B  Patrice O.  Patrice O.  Technologies, Inc.  Technologies, Inc.  Technologies, Inc.  US/08/WS-DOS  Task  Mmpatible  C-DOS/MS-DOS  TAs:  US/08/240,049B  TION:  US/08/240,049B	Hepatitis E Virus (Burma strain) ORF-2 10.0%; Score 3408; DB 1; Length 10.0%; Pred. No. 3.7e-294; re 0; Mismatches 0; Indels
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	T 1  12.240-049B-15  uence 15, Application US/082400 ent No. 5686239  wereal information: APPLICANT: Tam, Albert W. APPLICANT: Redbood City STREET: 505 Penclabs Technolo STREET: 505 Penclabs Technolo STREET: GA COUNTRY: WGA COUNTRY: WGA COUNTRY: WGA COUNTRY: WGA COMPUTER: ENDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS- SOFTWARE: Patentin Release # APPLICATION NUMBER: US/08/24 TELING DATE: OP-MAY-1994 CLASSIFICATION NUMBER: 38,615 REFERENE/POCKET NUMBER: 460 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (415) 324-0960 TOPOLOGY: linear MOLECULE TYPE: protein	TE: TE: 1( vativ
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100.0%; Score 3408; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.7e-294;
Matches 660; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 20,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                  PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
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                                                                          PFAPDVTAAAGAGPRVROPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
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APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.Shin
APPLICANT: Twudy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Heatitis B Virus Vaccine and Method
NUMBER OF SEQUENCES: 60
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Deblinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08259148A Patent No. 5741490 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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                 TOPOLOGY:
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                                                           LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                         Sequence 19, Application US/08484054

Patent No. 5770689

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reyes, Daniel W.
APPLICANT: Purdy, Michael W.
APPLICANT: Tam, Jr-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Heavezynski, Krzysztof Z.
ITILE OF INKERWACYNSKI, Krzysztof Z.
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 13-OCYCHER-1989
FILING DATE: 13-OCYCHER-1989
FRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 336,672
THING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
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FILING DATE: 16-JUNE-1989
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MEDIUM TYPE: Floppy
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US-08-484-054-19
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Fatent No. 5885768
GENERAL INFORMATION
APPLICANT: Reves, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCE: 76
CORRESPONDENCE ADDRESS:
ADDRESSES: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                          Length 660;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                       100.0%; Score 3408; DB 1;
100.0%; Pred. No. 3.7e-294;
ive 0; Mismatches 0;
                                                                                                ORF 2, BURMA, FIGURE
                                                                                                                                                                                                                                                Matches 660; Conservative
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: C
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481 DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540
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APPLICANT: Bradley, Daniel W
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tram, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6120988-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                          VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ
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SUFTRAINE STATEM:
SUFTRAINE STATEM:
SUBSTITEM:
APPLICATION NUMBER:
FILING DATE:
O'-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
IN 08/279,823
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATIO
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: 350 Cambridge Avenue, Suite 250
Palo Alto
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FILIND DATE: 13-0CT-1989
PRIOR APPLICATION DATA: 16-70N-1989
FILING DATE: 16-70N-1989
PRIOR APPLICATION NUMBER: US 07/36,672
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APPLICATION DATA: APPLICATION NUMBER: US 07/208,997
APPLICATION NUMBER: US 07/208,997
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Yarbough, Patrice O
Bradley, Daniel W
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: Reyes,
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                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSTETCENTON ...
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; INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE 9
US-07-876-941A-19
                                                                                                                                                                                                                                                                                                                               APPLICATION NOMBER 1992
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEFPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
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amino acid
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                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGGRGGGGGGFWGDRVDSQPFAIPYIHPTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis E Virus (Burma strain)
ORF-2
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
TELEFROME: (415) 324-0860
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 3408; DB 3;
100.0%; Pred. No. 3.7e-294;
tive 0; Mismatches 0;
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660 amino acids
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Matches 660; Conservative
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                               STATE: CA
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGEIGRGIALTLENLADTLIGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480
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                                            NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08542634
Patent No. 6214970
GENERAL INFORMATION:
APPLICANT: Perst, Thomas R.
APPLICANT: McAkee, C. Patrick
APPLICANT: Yarbough, Patrice O.
                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: 1:---
OLROW
          17-JUN-1988
                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-478-507-8
          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-542-634-13
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LENGTH: 660 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 660; Conservative
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Patent No. 6229005
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Bradley, Daniel W
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: No. 6229005-A/No. 6229005-B Hepatitis Viral Agent
                                             DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                         DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                   541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORPTURE: Batentin Release #1.0, Version #1.25
SOUTHARE: Batentin Release #1.0, Version #1.25
SOUTHARE: Batentin Release #1.0, Version #1.25
SOUTHARE: 03-40G 1998
FILING DATE: 03-40G 1998
FILING DATE: 25-40L-1994
FRILNG DATE: 25-40L-1994
FRILNG DATE: 15-50F, 888
FILING DATE: 05-40F, 1991
FRILNG DATE: 05-40F, 1991
FRILNG DATE: 05-40F, 1991
FRILNG DATE: 10-50T, 1989
FRILNG DATE: 11-50T, 1989
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0800
TELEPHONE: (650) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                       61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 300
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                                                                                  1 MRPRPILLLLIMFLPMLPAPPPGQPSGRRRGRRSGGSGGFWGDRVDSQPFAIPYIHPTN
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                                           Gaps
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Length 660;
                                         Indels
100.0%; Score 3408; DB 3; 100.0%; Pred. No. 3.7e-294;
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                                         0; Mismatches
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601 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL 660
                                                                               541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600
                                                                                                                                                                                                                                                                       APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Bradley, Daniel W
APPLICANT: Tawaczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6379891-A/No. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/err
FILING DATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: US/UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-UUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: US-APR-1990
PRIOR APPLICATION NUMBER: US 07/505,888
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 07/420,921
PRILING DATE: 13-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
                                                                                                                                                                                                            Sequence 8, Application US/09553427
Patent No. 6379891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE: 11-APR-1989
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TOPOLOGY:
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ORF-2
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 3408; DB 3;
Pred. No. 3.7e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,952
                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: G32P9
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415)369-9500
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                           FILING DATE
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   Length 660;
                                   Indels
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; Patent No. 6455492
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reves, Gregory R.
APPLICANT: Tew, Or-Shin
APPLICANT: Tew, Jr-Shin
APPLICANT: Tew, Jackin M.
APPLICANT: Tew, Albert W.
APPLICANT: Tew, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
   Score 3408; DB 4;
Pred. No. 3.7e-294;
0; Mismatches 0;
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350 Cambridge Avenue, Suite
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
      100.0%;
100.0%;
Query Match
Best Local Similarity 100.
Matches 660; Conservative
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STREET: 35
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                                                                                                                                        PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
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                                                                       1 MRPRPILLLLLMFLPMLPAPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN
                                        Gaps
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Patent No. 6432408

GENERAL INFORMATION

APPLICANT: MENG. XIANG-JIN

APPLICANT: Emerson, Suzanne U.

APPLICANT: Emerson, Suzanne U.

APPLICANT: EMERSON, SUZANG-JIN

APPLICANT: EMERSON, SUZANG-JIN

TITLE OF INVENTION: A SWINE HERATITIS E VIRUS AND USES THEREOF

FILE REFERENCE: 20264267US1

CURRENT APPLICATION NUMBER: US/09/462,606

CURRENT PILING DATE: 1997-07-18

PRIOR FILING DATE: 1997-07-18

PRIOR PILING DATE: 1997-07-18

PRIOR PILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 65

SOFTUM APPLICATION NUMBER: 1988-07-17

NUMBER OF SEQ ID NOS: 65

LENGTH: 660
                                        ô
          Length 660;
                                        Indels
      100.0%; Score 3408; DB 4;
100.0%; Pred. No. 3.7e-294;
ive 0; Mismatches 0;
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CRGANISM: Hepatitis E virus
US-09-462-606-50
          Query Match
Best Local Similarity 100.
Matches 660; Conservative
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US-09-462-606-50
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                                               421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAAEY
                                                                                                       DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
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                       QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis E Virus (Burma strain)
ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13703 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 3408; DB 5; 100.0%; Pred. No. 3.7e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application PC/TUS9513703 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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STATE: CA
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                   PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fabian, Gary R. 33,875
REGISTRATION NUMBER: 33,875
REFERENCE TUNBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                             FILING DATE: 20-APRIL-1992
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION MINIOR
                                                                                                                                                                                            APPLICATION DAIA:

FILING DATE: 05-APRIL-1990

RRIOR APPLICATION DATA:

APPLICATION NUMBER: US 420, 921

FILING DATE: 13-OCTOBER-1989

PRIOR APPLICATION NUMBER: US 367, 486

FILING DATE: 16-UUME-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 336, 672

FILING DATE: 11-APRIL-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 208, 997
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 660 amino acids
                 SOFTWARE: Patentin Rel.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Best Local Similarity 100.
Matches 660; Conservative
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US-07-870-985A-19
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                      121 PVPDVDSRGAILERQYNLSTSPLTSSVARGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                        ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL
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                                                           NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
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99.5%; Score 3391; DB 4;
Best Local Similarity 99.4%; Pred. No. 1.2e-292;
Matches 656; Conservative 1; Mismatches 3;
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Batent No. 6432408

GRERAL INFORMATION:
APPLICANT: MENG. XIANG-JIN
APPLICANT: Emerson, Suzanne U.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRU;
FILE REFERENCE: 20264267USI
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
RIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-17
SOFTWARE: PATENTIN NUMBER: PCT/US98/14665
SOFTWARE: PATENTIN NUMBER: PCT/US98/14665
SOFTWARE: PATENTIN NUMBER: PCT/US98/14665
SOFTWARE: PATENTIN ON SEQ. ID NOS: 65
SOFTWARE: PATENTIN ON SEC. 2.1
SEQ. ID NO 12.
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APPLICANT: Anderson, David A.
APPLICANT: Locarnini, Stephen A.
APPLICANT: Locarnini, Stephen A.
APPLICANT: Toressi, Joseph
APPLICANT: Hui, Zhuang
APPLICANT: Hii, Fan
TITLE OF INVENTION: IMMUNORBACTIVE ANTIGENS OF HEPATITIS E VIRUS
FILE REFERENCE: Davies CO. Cave
CURRENT APPLICATION NUMBER: US/09/172,699A
CURRENT APPLICATION NUMBER: 08/617,927
BARLIER PILING DATE: 1996-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Pred. No. 2.3e-293;
1; Mismatches 1; Indels
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Matches 658; Conservative
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US-09-172-699-2
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APPLICANT: Esarev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And J
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,316
FILING DATE: 11-ARR-1997
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Patent No. 6054567
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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USA
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Pred. No. 7.6e-292;
2; Mismatches 3;
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                                                                                          residues
                                                                                                                                                                                                                            99.2%;
(212) 758-4800
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 660 amino acid re: TYPE: amino acid acid STRANDEDNESS: unknown
                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.2
Matches 655; Conservative
                                                                                                                                    STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                               US-08-840-316-2
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Blank Sheet

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August 16, 2004, 13:35:07; Search time 51 Seconds (without alignments) 4062.587 Million cell updates/sec
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1 MRPRPILLLLLMFLPMLPAP.....QSTVAELQRLKMKVGKTREL 660
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1292805 seqs, 313927144 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 13, Appl	Sequence 8, Appli	Sequence 19, Appl	Sequence 1, Appli					Sequence 51, Appl		Sequence 55, Appl		92,	167,	Sequence 167, App
		ID	US-09-769-066-13	US-09-851-410-8	US-10-165-868-19	US-10-381-770-1	US-10-257-044-1	US-09-769-066-14	US-10-165-868-20	US-10-239-090A-57	US-10-239-090A-51	US-10-239-090A-53	US-10-239-090A-55	US-09-468-147-92	US-10-319-745-92	US-09-468-147-167	US-10-319-745-167
		DB	σ	10	14	12	15	σ	14	16	16	16	16	10	12	10	12
		Match Length DB	999	099	099	099	099	099	629	674	099	099	674	099	099	099	099
₩	Query	Match	100.0	100.0	100.0	99.5	99.3				93.2						
		Score	3408	3408	3408	3391	3383	3221	3194.5	3179	3176	3174	3166	3160	3160	3151	3151
	Result	No.	٦	71	e	4	Ŋ	9	7	80	თ	10	11	12	13	14	15

NAME: Fabian, Gary R.
REGISTRATION UNDRER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880 TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 13:

Sequence 15, Appl Sequence 27, Appl Sequence 26, Appl Sequence 16, Appl Sequence 28, Appl Sequence 28, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 206, Appl Sequence 207, Appl Sequence 206, Appl Sequence 199, Appl Sequence 199, Appl Sequence 116, Appl Sequence 1189, Appl Seq	
US-09-769-066-15 US-09-769-066-25 US-09-769-066-27 US-09-769-066-26 US-09-769-066-26 US-09-769-066-18 US-10-165-868-18 US-10-165-868-18 US-10-165-868-18 US-10-165-868-18 US-10-165-868-18 US-10-165-868-18 US-10-165-868-18 US-10-19-745-207 US-10-319-745-207 US-10-319-745-207 US-10-319-745-199 US-10-319-745-199 US-10-319-745-176 US-10-319-745-176 US-10-319-745-176 US-10-319-745-176 US-10-319-745-176 US-09-468-147-176 US-09-468-147-176 US-09-468-147-175 US-09-468-147-175 US-09-468-147-175 US-09-468-147-175 US-09-468-147-175 US-09-468-147-175	US-10-381-770-4 US-10-381-770-12 US-10-381-770-2
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2813 2669 2669 26694 26684 2009 2009 2009 2009 2009 2009 2009 200	100
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ALIGNMENTS

APPLICANT: Fuerst, Thomas R.
MCALCE, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGENS AND USES THEREFOR CORRESPONDENCES 31
CORRESPONDENCE ADDRESS: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SERATURO SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 250 ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Ave., Suite CITY: Palo Alto APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/542,634
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION: Sequence 13, Application US/09769066 Patent No. US20020107360A1 GENERAL INFORMATION: CURRENT APPLICATION DATA: COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM: STATE: CA US-09-769-066-13

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US20030124510A1-A/No. US20030124510A1-B Hepatitis Vira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRPRPILLLLLLMFLPMLPAPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFALPYIHPTN
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                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 3408; DB 10;
100.0%; Pred. No. 7.9e-276;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 4600-0183.24
                                                                              STREET: 350 Cambridge Avenue, Suite CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                 PREDICATION DATAS.

PRELICATION DATAS.

FILING DATE: 07-May-2001

PRIOR APPLICATION DATAS.

PRILICATION NUMBER: 09/128,275

FILING DATE: 4DARNOWD.

APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1990

APPLICATION NUMBER: US 07/420,921

FILING DATE: 13-0CT-1989

APPLICATION NUMBER: US 07/420,921

FILING DATE: 16-DAN-1989

APPLICATION NUMBER: US 07/367,486

FILING DATE: 16-DUN-1989

APPLICATION NUMBER: US 07/367,986

FILING DATE: 11-APR-1989

APPLICATION NUMBER: US 07/36,672

FILING DATE: 11-ADN-1989

APPLICATION NUMBER: US 07/208,997

FILING DATE: 11-ADN-1989

APPLICATION NUMBER: US 07/208,997

FILING DATE: 11-ADN-1988
                                                                   Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;

MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-851-410-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Petithory, Joanne R. REGISTRATION NUMBER: 42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 660 amino acids
                                                                 ADDRESSEE: Dehlinger &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS
    No.
                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Marches 660; Conservative
                                                                                                                                                      COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360
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                                                                 STRANDEDNESS: Hepatitis E Virus (Burma strain)
                                                                                                                                                                                                                                                         Score 3408; DB 9;
Pred. No. 7.9e-276;
; Mismatches 0;
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                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
ONGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-769-066-13
                        LENGTH: 660 amino acids TYPE: amino acid
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ilarity 100.0%;
Conservative 0
    SEQUENCE CHARACTERISTICS:
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                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  Similarity
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Best Local Simi
Matches 660;
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ORF 2, BURMA,
2 ID NO: 19:
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           INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 660 amino acids
                                                                                                                                         INDIVIDUAL ISOLATE: O:
; SEQUENCE DESCRIPTION: SEQ US-10-165-868-19
                                                                                                                                                                                                  100.0%;
al Similarity 100.0%;
660; Conservative 0;
                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                       TYPE: amino acid
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 660; Conserv
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US-10-381-770-1
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                                                                                                    QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R. 3 REGISTRATION UNBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/07/870,985A FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
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APPLICATION WUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
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US-10-165-868-19
Sequence 19, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R. Twu, Jr-Shin
Purdy, Mchael A. Furd, Mchael A. Furd, Albert W. Tam, Albert W. Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
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ZIP: 94306
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Sequence 1, Application US/10381770

Sequence 1, Application US/20040052813A1

GENERAL INFORMATION:
APPLICANT: YANG SHENG TANG company, Ltd.
APPLICANT: YANG SHENG TANG company, Ltd.
TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOSTITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REPERENCE: IECO10037PCT
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                                                                                                                                                                 Indels
                                                                                                          Score 3408; DB 14; Pred. No. 7.9e-276; 0; Mismatches 0;
FIGURE
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/ No. US20030220475Ale
OTHER INFORMATION: Synthetic construct
US-10-257-044-1
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MCAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HPPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                               Ouery Match 99.3%; Score 3383; DB 15; Best Local Similarity 99.4%; Pred. No. 9.7e-274; Matches 656; Conservative 2; Mismatches 2;
                                                     4.0
PRIOR APPLICATION NUMBER: 60/195,380 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 LENGTH: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
                                                                                                                      ORGANISM: Artificial Sequence
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Publication No. US20030220475A1
Publication No. US200210475A1
Publication No. US2002104A1
Publication Represented by the Secretary, Department of Health and APPLICANT: HOWARD A. FIELDS
APPLICANT: HOWARD A. FIELDS
APPLICANT: JIHONG MENG
APPLICANT: JIHONG MENG
TITLE OF INVERTION: NEUTRALIZING IMMUNOGENIC HEV POLYPEPTIDES (HEV)
FILE REFERENCE: 14114.034902
CURRENT APPLICATION NUMBER: US/10/257,044
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                                                                                                                                                         Score 3391; DB 12;
Pred. No. 2.1e-274;
1; Mismatches 3;
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   2003-07-16
                                                                                                                                                       Query Match
Best Local Similarity 99.4%;
Matches 656; Conservative
                                                                                                       ORGANISM: hepatitis E virus
CURRENT FILING DATE: 2003-
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version
SEQ ID NO 1
                                                                      099
                                                                                                                        US-10-381-770-1
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421 ODKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480
                                          DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                                             541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                       541 LRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAGPVAISAAAV
                                                              481 DQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDMSKVTLDGRPLPTVEQYSKTFFVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SECHENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
APPLICATION NUMBER: US 336,672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/165,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reyes, Gregory R. Bradley, Daniel W. Twu, Jr. Shin Purdy, Michael A. Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 659 amino acids
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                            COMPUTER: LEAD FOUND.

COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFCATION NUMBER: 08/542,634
FILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: 08/542,634
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0293.30
TELEPHONE: (412) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ORF-2
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Best Local Similarity 93.5%; Pred. No. 3.4e-260;
Matches 617; Conservative 21; Mismatches 22;
             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHERICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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INFORMATION FOR SEQ ID NO: 14:
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LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                          ZIP: 94306
COMPUTER READABLE FORM:
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                                                                                                        USA
                                                                                                      COUNTRY:
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DEPLICANT: KABUSHIKI KAISHA TOSHIBA
TITLE OF INVENTION: Polymucleotide probe and primer derived from hepatitis E virus co
TITLE OF INVENTION: From Japanese, chip including the same,
TITLE OF INVENTION: from Japanese, chip including the same,
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REFERENCE: 0280741P
CURRENT APPLICATION NUMBER: US/10/239,090A
CURRENT FILING DATE: 2003-07-24
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 5:
LENGTH: 660
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                                                                                                              15 MRSRALLFLFVFLFWLPAPPAGQPSGRRRGRRSGGAGGFWGDRVDSQPFALPYIHPTN
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                                674;
                              Length
                                                                Indels
                              93.3%; Score 3179; DB 16; 92.1%; Pred. No. 1.1e-256;
                                                              25; Mismatches
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; Publication No. US20040101820A1
; GENERAL INFORMATION:
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                                                              607; Conservative
                                               Similarity
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US-10-239-090A-57
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                                                                              Score 3194.5; DB 14;
Pred. No. 5.6e-258;
1; Mismatches 24; I
                 FIGURE
                 MEXICO,
                 2, NO:
               INDIVIDUAL ISOLATE: ORF
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                              21;
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llarity 93.0%;
Conservative 21
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                                                 US-10-165-868-20
                                                                                                                614;
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RESULT 11

US-10-239-000A-55

Sequence 55, Application US/10239090A

Sequence 55, Application Ws. US20040101820A1

GENERAL INFORMATION:
TULL CALL OF INVENTION: FOLYMUCIECTICE probe and primer derived from hepatitis B virus co.
TITLE OF INVENTION: from Japanese, chip including the same, kit including the same,
TITLE OF INVENTION: detecting hepatitis E virus using the same
TITLE OF INVENTION: detecting hepatitis E virus using the same
CURRENT APPLICATION NUMBER: US/10/239,090A

CURRENT FILING DATE: 2003-07-24

REIOR PERIOR PRINC DATE: 2001-66-25

NUMBER OF SEQ ID NOS: 57

FEASO ID NOS: 57

FEASO ID NOS: 57
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                                                       PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
                                                                                                             PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                                                                                                                   NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
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US-10-239-090A-55
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Sequence 53, Application US/10239090A
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Sequence 53, Application US/10239090A
Sequence 53, Application US/10239090A
Sequence 53, Application US/1020A
Sequence 53, Application US/1020A
Sequence 53, Application US/1020A
TITLE OF INVENTION: From Japanese, Chip including the same, RITLE OF INVENTION: detecting hepatitis E virus using the same, TITLE OF INVENTION: detecting hepatitis E virus using the same, TITLE OF INVENTION: detecting hepatitis E virus using the same, CURRENT FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: JP2001-191837
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 57
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 Pred. No. 2e-256;
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 al Similarity 92.1%; Pro 607; Conservative 26;
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Matches 607; Conservative
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APPLICANT: ADDOTT Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: MARANAEV. I. K.
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HOWBER: US/10/319,745
CURRENT FILING DATE: 2002-12-13
FRIOR PAPLICATION NUMBER: US/09/468,147A
PRIOR PILING DATE: EABLIER FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/061,199
PRIOR PILING DATE: EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
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  DB 10;
92.7%; Score 3160; DB 10;
91.7%; Pred. No. 4.3e-255;
cive 27; Mismatches 28;
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Query Match
Best Local Similarity 91.7%
Matches 604; Conservative
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APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Brker, James C.
APPLICANT: Brker, James C.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: HEPATITIS E VIRUS
THER PETENT APPLICATION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1997-10-15
EARLIER FILING DATE: 1997-10-15
SEQLID NO 92.
TENDOR SEQ ID NOS: 258
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FEATURE:
OTHER INFORMATION: Xaa = Unknown or Other at
OTHER INFORMATION: Xaa = Unknown or Other at
OTHER INFORMATION: Xaa = Unknown or Other at
US-09-468-147-92
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Pred. No. 2.4e-254;
6; Mismatches 30;
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at
FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEO ID NOS: 258
SOFTWARE: FASCEQ for Windows Version 3.0
SEQ ID NO 167
                                                                                                                                                                                                                                                                  Query Match
92.5%; Score 3151; D
Best Local Similarity 91.5%; Pred. No. 2.4e
Matches 603; Conservative 26; Mismatches
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US-10-319-745-167
US-10-319-745-167
; Sequence 167, Application US/10319745
; Publication No. US20030211467A1
; GENERAL INFORMATION:
                                                                                                                                                           TYPE: PRT
ORGANISM: Hepatitis E Virus
FEATURE:
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APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Exter, James C.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
IITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
                                                                                      OTHER INFORMATION: Xaa = Unknown or Other at position 481 OTHER INFORMATION: Xaa = Unknown or Other at position 542 OTHER INFORMATION: Xaa = Unknown or Other at position 595 US-10-319-745-92
                                                                                                                                                                                    Indels
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            3.0
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           Version
           Windows
                                                              ORGANISM: Hepatitis E Virus
                                                                                                                                                      Query Match
Best Local Similarity 91.74
Matches 604; Conservative
           for
         SOFTWARE: FastSEQ
SEQ ID NO 92
LENGTH: 660
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APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: HERAITIES E VIRUS
TITLE OF INVENTION: DATE: 202-10.5P1
CURRENT APPLICATION NUMBER: US/09/468,147A
PRIOR PILING DATE: 1999-1-2-21
PRIOR PLING DATE: BARLIER FILING DATE: 1998-10-15
PRIOR PLING DATE: EARLIER FILING DATE: 1999-10-15
PRIOR PLING DATE: EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Windows Version 3.0
SERVICENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.5%; Score 3151; DB 12;
Best Local Similarity 91.5%; Pred. No. 2.4e-254;
Matches 603; Conservative 26; Mismatches 30;
                Schlauder, George G.
Erker, James C.
Desai, Suresh M.
   APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Hepatitis E Virus
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                  APPLICANT:
APPLICANT:
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Aar96103 |
Aar70323 |
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Abj04803
Aar91814
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Abb81670 1
Ada50060 1
Adb97807 1
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 -MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPFO spool_p/USOSB81410/runat_16082004_125716_9617/app_query.fasta_1.4238
-DE=A_Geneseq_29Jan04 -OFMT=fastan -SUFFIX=oli.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=A5 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HARPSIZE=500 -MINIEN=0 -MAXLEN=200000000
-USR=USOSB51410_@CGN_1_1_141_@runat_16082004_125716_9617 -NCPU-6 -ICPU=3
-NO_MMAP -LARREDUERY -NEG-SCORES=0 -MAINT -DSPBLOCK=100 -LONGLOG
-DBY TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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Aar56089 Hepatitis
Aaw35826 Hepatitis
Aaw80137 Protein e
Aaw93389 Human HEV
Aab54120 Hepatitis
Aab562523 HEV-Burma
Aao15699 Hepatitis
Add24376 Hepatitis
                                                                                               August 16, 2004, 13:35:43 ; Search time 89.8179 Seconds (without alignments) 12476.164 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                          US-09-851-410A-6_COPY_5147_7129
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p 60.0 , Ygapext 60.0
p 6.0 , Fgapext 7.0
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AAR96089
AAW35826
AAW80197
AAB24120
AAB24120
AAB24223
AAB65523
AAD624376
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geneseqp2003as:*
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                                                                               immunogenic hepatitis E virus (HEV) peptide(s) - are from and ORF3 regions of HEV, useful as a vaccine against HEV
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                                                                                                                                                                                       GInSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu
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TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla
                       ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
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HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                                                                      Hepatitis E virus (HEV) antigens derived from ORP 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
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Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                      (GENE-) GENELABS TECHNOLOGIES INC.
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                                                                         Burma strain,
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95US-00542634.
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                                                                         Hepatitis E virus;
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                                                                361 ValGlyGlulleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeu
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                  LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGly
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TyrasnThrThralaSerAspGlnLeuLeuValGluAsnAlaAlaAlaGlyHisArgValAla
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                                                        GITAATGITGCGACCGGCGCGCAGGCCGTTGCCCCGGTCGCTCGATTGGACCAAGGTCACA
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920S-0082335.
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                       AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn
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A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents the protein from the open reading frame, ORF2, from HEV Burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-field)
                                          Diagnosis of hepatitis E virus Burma and Mexico strain infection - by immunoassay with hepatitis E virus peptide antigens.
                                                                                                      Disclosure; Col 39-42; 36pp; English.
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Sequence 660 AA;

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Burma HEV isolate; vaccine; diagnostic
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23-DEC-1998
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16-JUN-1989;
13-OCT-1989;
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Pred. No.:
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Human HEV ORF 2 protein from strain Burma

(first entry)

11-JUN-1999

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ValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeu
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                                 CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
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mutants which are capable of cross rescting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in vaccines for immunishing against HEV infection. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a swine hepatitis E virus (HEV) and its natural
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                                                                                                                                                                                                                                                                                                                         New isolated swine hepatitis E virus - used to develop products for diagnosis, prevention and treatment of hepatitis E virus infection mammals, particularly humans.
                                                   hepatitis E virus; HEV; cross-reaction; antibody; human; le; immunise; infection; detection; diagnosis; prevention.
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Gaps:
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                                                                                              Hepatitis E virus.
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PropheAlaProAspValThrAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla

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standard; protein; 660

AAW93389

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(GENE-) GENELABS TECHNOLOGIES INC. (USGO ) US GOVERNMENT.
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Reyes GR; Tam A, Bradley DW, Yarbough PO, Krawczynski KZ, Fry KE,

WPI; 2000-593712/56. N-PSDB; AAA99259.

Identifying recombinant antigen immunoreactive with antibody induced by hepatitis E virus (HEV), for detecting HEV infection, comprises immunoreacting a polypeptide from an HEV genome with an HEV-positive antiserum.

Claim 6; Col 63-68; 46pp; English.

The present invention describes a method for identifying a recombinant antigen immunoreactive with a hepatitis B virus (HEV)-induced antibody. The method comprises producing a polypeptide derived from an HBV genome, immunoreacting the polypeptide with an HBV-positive antiserum and selecting the polypeptide as a recombinant antigen if the polypeptide reacts with the HBV-positive antiserum. The method is useful for identifying recombinant antigen immunoreactive with antibody induced by HBV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also known as HBV))-specific fragments are useful for identifying ET-NANB. Whom as HBV) specific fragments are useful for identifying ET-NANB viral genomic material in a patient sample, for the synthesis of polypeptides for use in immunoassays, and for identifying synthesis of polypeptides for use in immunoassays, and for identifying similar antispenic regions encoded by related viral strains, e.g. Burmese strain. The antigens are especially useful in the preparation of vaccine against ET-NANB infection. These antigens may further be used to prepare antiodies to ET-NANB virus particles for use directly as antiviral agents, and to produce antiserum designed for pre- or post-exposure prophylaxis. The present sequence represents a specifically claimed HEV Burma strain protein sequence for use in the present invention

Sequence 660 AA

		0.9	20	120	40	180	09	240	80	300	100	360	120	420
660 660 660 8: 0	120 (1-660)	ATGCGCCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGCGCCA		CCGCCCGGTCAGCCGTCTGGCCGTCGTGGGGCGCGCAGCGGCGGGTTCCGGCGGTGGT		TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA		GGCTGGACCTCGTGTTCGCCAACCCGCC	ProPheAlaProAspValThrAlaAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla	CGACCACTCGGCTCCGCTTGGCGTGACCAGCCCCAGCGCCCCGCCGTTGCCTCACGTCGT	ArgProLeuGlySerAlaTrpArgAspGlnAlaGlnArgProAlaValAlaSerArgArg	AGACCTACCACAGCTGGGGCGCGCGGTAACCGCGGTCGCTCGGCCCCATGACACCCCG	ArgProThrThrAlaGlyAlaAlaProLeuThrAlaValAlaProAlaHi8AspThrPro	CCAGTGCCTGATGTCGACGCTCCGCGGCGCCTTGCGCCGGCAGTATAACCTATCAACA
Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-1983) x AAB24120	TTTGTTGCTGCTCCTCAT		rescescercerceresco	GlyArgArgArgGlyAr	GATTCTCAGCCCTTCGC	PheTrpGlyAspArgValAspSerGlnProPheAla1	CTGCGGCCG		rTGGCGTGACCAGGCCC	aTrpArgAspGlnAlaGl	GCCGCCCCCTAACCCC	AlaAlaProLeuThrAl	CTCCCGCGCGCCATCT
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Db	121	ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140
ογ	421	TCTCCCCTTACCTCTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCCTCTT 480
Dp	141	SerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProLeu 160
č da	481	481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540
3 3	1 4 5	AATTATGCCAGTTGCCGGGTTGCCCACAATCGCCGCCGCCGCCGCCCCAAT 600
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δ	601	GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACACACCACCACCACCGGACG 660
Dp	201	AlaValGlyGlyTyrAlalleSerIleSerPheTrpProGlnThrThrThrThrThrProThr 220
à à	661	TCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720
3 3	721	Servataspmerasinseriletiniserilnikaspvalargileteuvaldinikoolyile 240 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780
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à	781	GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTA 840
Dp	261	ValGluThrSerGlyValAlaGluGluAlaThrSerGlyLeuValMetLeuCyslle 280
Š	841	CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 900
qq	281	HisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 300
දි දි	901	GACTITGCCCTTGAGGTTGGCAACCTTACCCCGGGTAACACCAATACGCGGGTC 960
an i	301	Asprnealaleuglukneargasnleulnrrroglyasninrasninrargval 320
<u>ک</u> ک	961	TCCCGTTATTCCAGCACTGCTCGCCACGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG
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· 音	341	LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGly 360
ζ	1081	GTCGGTGAGATCGGCCGCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT 1140
Db	361	ValdiyGluileGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeu 380
λ	1141	GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC 1200
Db	381	GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlnLeuPheTyrSerArgPro 400
بې دې	1201	GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
3 3	104	VAIVALOETRIARBIIGTÄGENKIOOIIIE VAILÄVBURULÄYLIILOGILVALGEURABIIGTÄÄRÄRÄNIN 200 CACCARAACORRAARPORAARPOOORAGACARAARPOROOOROOROOROOROARAARPOOPOOROARAARPOOPOOROARAARPOOPOOROOROOROOROOROOROOROOROOROOROOROO
S &	421	CAGGAINAGGGIAILGCAALCCCCAIGACAILGACCLCGGAGAAICICGGGGGGGAIT 1320 
λ	1321	CAGGATTATGATAACCAACATGAACAACATGGGCGGCGGCGCCCTTCTCCAGCCCCATCGCGC 1380
qq	441	
٥٧	1381	CCTITCTCTGTCCTTCGAGCTAATGATGTGCTTTTGGCTCTCTCT
qq	461	ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 480
à à	1441	GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTATGTTTCTGACTCTGTGACCTTG 1500
Q O	481	ASPGINSETINTIYTGIYSETSETINTGIYKTOVALIYIVALSELASPSETVALINLLEGG 500

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The invention relates to an isolated DNA comprising the genome of an referrically transmitted nonA/nonB (ET-NAMB) viral hepatitis agent (also referred as HEV). The DNA sequences or their fragments are useful in preparing ET-NAMB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NAMB virus), as well as in vaccine production. The Present sequence represents a ORF2 protein encoded by a ET-NAMB viral DNA sequence from HEV-Burma strain
  in vaccine production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheTrpGlyAspArgValAspSerGlnProPheAla1leProTyr11eHisProThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCC
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                GITAATGITGCGACCGCGCGCAGGCCGTTGCCCCGGTCGCTCGATTGGACCAAGGTCACA
                                        CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACGTCTTTGTCCTGCCG
                                                                                                                   TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
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                                                                                                                                                                                                                                                                                                                                ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGT
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90US-00505888.
91US-00681078.
94US-00279823.
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89US-00367486.
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ET-NANB; infection; vaccine
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N-PSDB; AAF83495
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05-APR-1991;
25-JUL-1994;
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16-JUN-1989;
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CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in bile samples from infected humans and monkeys using polymerase chain reaction.
                                                                                                CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC
                                                                                                                                                                                                                                                                transmitted nonA/nonB hepatitis viral agent;
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Matches:
Conservative:
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89US-00336672.
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PO,
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Burma strain; bile; ORF2
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16-JUN-1989;
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05-APR-1990;
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25-JUL-1994;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                           New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis viral agent.
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Matches:
Conservative:
Mismatches:
Indels:
                        HEV;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 8; 81pp; English
                        hepatitis; ET-NANB;
 Burma ORF
                                                 Burma
                                                                                                                                               88US-00208997.
89US-00336672.
89US-00420921.
90US-00505888.
91US-00681078.
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N-PSDB; ADD24374.
                                                 E virus;
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11-APR-1989;
16-JUN-1989;
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05-APR-1990;
05-APR-1991;
25-JUL-1994;
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This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible
                                                                                                                                                                                                                                                                                  ArgProThrThrAlaGlyAlaAlaProLeuThrAlaValAlaProAlaHisAspThrPro
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Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, immuno-assays and nucleic acid hybridisation.
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                                            Claim 13; Page 24-26; 29pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterically transmitted nonA/nonB hepatitis virus; identification; HEV; ET-NANB; detection; vaccine.
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62K antigen (AAR96091) comprises the C-terminal 549 amino acids of Phepatitis E virus (HEV) Burma strain capsid protein (see also AAR96089). It is obtd. by PCR amplification of HEV Burma ORF-2 (AAT27107), insertion of amplified DNA (AAT27109) into vector pGBX and expression in B. coll cells. Expression of full-length ORF-2 in Sf9 insect cells using a baculovirus system also results in prodn. of 62K antigen (see also AAR96103). 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                         Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines
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                                                             Hepatitis E virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a neutralising hepatitis E virus (HEV) polypeptide comprising C-terminal of HBV pORF2 protein containing at least one neutralising epitope. HEV is a non-enveloped virus. HEV polypeptide is useful for studying the pathogenesis of HEV and monitoring treatment efficacy in subjects undergoing treatment for HBV. The polypeptide is used as a reagent to detect HBV and as a vaccine to treat or prevent HEV infection. The present sequence is HBV long capsid protein encoded by open reading frame 2, also referred as pORF2
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                                                                                Location/Qualifiers
221. .660
/note= "This region contains P1-P51 overlapping synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal portion of the pORF2 protein of hepatitis E virus polypeptide containing a neutralizing epitope, useful to detect, prevent and treat hepatitis E virus infections.
          ProvalSerIleSerAlaValLeuAlaProHisSerAlaLeuAlaLeuClu
                                            GATACCTIGGACTACCCTGCCCGCGCCCATACTTIGATGATTCTGCCCAGAGTGCCGC
                                                                                                                                                                                                                                     Hepatitis E virus; HEV; capsid protein; antiviral; vaccine; therapy;
                                                                                                                                                                                                                   Hepatitis E virus ORF2 encoded long capsid protein
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                                                                                                                   AAE12980 standard; protein; 660 AA.
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DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus (HEV) Burma strain capsid protein was cloned into baculovirus expression vector pabluaecill and recombinant 62K was expressed in Sf9 insect cells. High levels of expression were obtd, and the recombinant 62K was obtd. in over 95% purity. However, C-terminal processing resulted in the deletion over 95% purity. However, C-terminal processing resulted in the deletion of 9 or 23 amino acids from 62K, giving 2 related polypeptide species (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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      nbv; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
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in vaccines.
                                                                                                                                                                                                                                                                                                                                                  antigens derived from ORF 2 - determining HEV infection and
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Mismatches:
Indels:
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                                                                               Burma strain
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95US-00542634.
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                                                                               Hepatitis E virus;
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Best Local Similarity:
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13-0CT-1995;
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ID AAR:
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101	InThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 12
694	GTTCGTATTTTRGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCCAAGTGAGCGCCTA 753 
754	CACTATEGTAACCAAGGETGGCGCTCCGAGACCTCTGGGGTGGCTGAGGAGGCT 813 
814	ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873 
874	CCCTATACCGGTGCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933 
934	ACCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993 
994	CGTCGCGGTGCGGACGGGACTGCCGACGCCACGGCTGCTACCCGCTTTATGAAG 1053 
1054	GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGGATAGCCCTCACC 1113
1114	CIGITCAACCTIGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATGATTTCGTCGGCT 1173 
1174	GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCCAGCCGACTGTTAAG 1233 
1234	TIGIAIACATCIGIRAGAGAATGCICAGCAGGATAAGGGIATIGCAATCCCGCATGACATT 1293 
1294 321	GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353 
1354	CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTGTGTCCTTCGAGCTAATGATGTGCTT 1413 
1414 361	TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTTCCACTTATGGCTCTTCGACTGGCCA 1473 
1474	GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCGC
1534	CGGTCGCTCGATTGGACCAAGGTCACCTTGACGGTCGCCCCTCTCCACCATCCAGCAG 1593
1594	TACTCGAAGACCTTCTTTGFCCTGCCGCTCCGCGGTAAGCTCTTTTTTGGGAGGCAGGC 1653 
1654	ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713
1714	GAGAATGCCGCCGGCCCCGCTCCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

CCCGTCTCCATTTCTGCGGT.	1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833	481 ProvalSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGlu 500	1834 GATACCTIGGACTACCCTGCCCGCGCCCATACTITIGATGATTTCTGCCCAGAGTGCCGC 1893	AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520	1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953	521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
	CCCGTCTCCATTTCT	ProvalSerIleSer	GATACCTTGGACTAC	AspThrLeuAspTyr	CCCCTTGGCCTTCAG	ProLeuGlyLeuGln
	δλ	qa	ò	qq	ò	qq

Search completed: August 16, 2004, 13:47:46 Job time: 126.818 secs

Rank Sheet

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Structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.; Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral: Reference number: A40778; MUID:92024067; PMID:1926770
A;Recession: C4078
A;Rocession: C4078
A;Residues: 1-660 A:TAM>
A;Residues: 1-660 A:TAM>
A;Residues: Les monmic RNA
A;Cross-references: GB:M73218; NID:9330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;22-660/Product: structural protein 2 #status predicted <SIG>F;23-660/Product: structural protein 2 #status predicted <SIG
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heme ABC transport
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Conservative:
Mismatches:
Indels:
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C97488
D82555
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T12366
T17053
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F96680
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T23797
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A87184
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-MODEL=frame+ n2p.model -DEV=xlp

-MODEL=frame+ n2p.model -DEV=xlp

-Q=/Capl 1/UGF70 spool p/US09851410/runat 16082004 125717 9653/app_query.fasta_1.4238

-Q=/Capl 2/UGF70 spool p/US09851410/runat 16082004 125717 9653/app_query.fasta_1.4238

-DB=PIR 78 -OFWT=fastan -SUFFIX=011.rpr -WINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=Dits -START=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto

-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000

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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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                                                                                                                                   August 16, 2004, 13:40:03 ; Search time 31.2737 Seconds
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                               using frame_plus_n2p model
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FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

pirl:\* pir2:\* pir3:\*

PIR\_78:\*

Database

SUMMARIES

Length

Query Match

Score

Result Š. 100.0 18.2

B44212 VHWWHE C44212 B40236 B86242 T12281

660 659 123 123 41 337 348 840

F83928 H58208

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819708

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Total number of hits satisfying chosen parameters:

Word size:

Searched:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

283366 segs, 96191526 residues

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Scoring table:

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		Ov 1441 GACCAGTCCACTTATGGCTCTTCGACTC
δλ	361 CCAGTGCCTGATGTCGACTCCCGCGGCGCCATCTTGCGCCGGCAGTATAACCTATCAACA 420	
qa	121 ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140	Db 481 AspGlnSerThrTyrGlySerSerThrC
ò	421 TCTCCCCTTACCTCTTCCGTGGCCACGGCACTAACCTGGTTCTTTATGCCGCCCCTCTT 480	Qy 1501 GTTAATGTTGCGACCGCGCGCAGGCCG
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qa	161 SerProLeuLeuProLeuGlnAspGlyThrAsnThrHislleMetAlaThrGluAlaSer 180	521
ò	541 AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCTGGTCCCCAAT 600	OY 1621 CTCCGCGGTAAGCTCTCTTCTGGGAGG
qq	181 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 200	1 60
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QQ	201 AlaValGlyGlyTyrAlaileSerIleSerPheTrpProGlnThrThrThrThrProThr 220	100
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ò	721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780	
qq	241 AlaSerGluLeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 260	1861
ઠે 1	GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA	
ad <u>.</u>	61 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle	Qy 1921 CAGTCTACTGTCGCTGAGCTTCAGCGCC
ð á	841 CATGGCTCACTGGTAAATTCCTATACTAATACACCCTATACGGTGCCCTCGGGCTGTTG 900	
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\$ A		C;Accession: B44212 R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Viralogy 191 550.558 1992
} ;	ntores of the control	A:Title: Molecular cloning and sequencing
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3 6	- Jefferstander der der der der der der der der der	A; Residues: 1-659 < HUA>
ර් ප්	101 GICGGIGHANNIGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	A;Cross-reterences: GB:M/4506; M.D.:g33001/ C;Superfamily: hepatitis E virus structura C:Revwords: structural protein
è	からかませいことは、本色の出土の住のできないのでは、からいまでは、大きのは、大きのは、大きのは、大きのは、大きのは、大きのできない。	F;1-22/Domain: signal sequence #status pre
ž 8	GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlyGlpLeuPheYyzSerArgPro	Alianment Scores:
è	GTTGTCTCAGCCAATGGCCGACTGATTAAAGTTGTAAAACTTGTAAAAAAAA	Pred. No.: 2.05e-109 Len
λ.	GIIGICICAGCCANIGGCGGGCCGGCIGIIAAGIIGINACAICIGIAGAAIGCICAG	00.021

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٥٨	1261	CAGGATAA	GGGTATTGCAATCCC	GCATGACATTGACC	CGGAGAATCTCGTGTGGTTATT	1320
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පි සි	1321	CAGGATTA	CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTT	ACAAGATCGGCCGAC	GCCTTCTCCAGCCCCATCGCGC	- Μ
ĝ	4	GIDASDIY	raspasneinhisei	JGI NASPARGPROTI	irProserProAlaProserArg	9
දු දු	1381	CCTTTCTC          ProPheSe	TGTCCTTCGAGCTAA	IGATGTGCTTTGGCT	CCTITCTCTGTCCTTCGAGCTAATGATGTGTTTTGGTTCTCTCACGCTGCCGGTAT 	1440
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ò	1501	GTTAATGT	TGCGACCGGCGCGCA	3GCCGTTGCCCGGTC		1560
qq	501	ValAsnVa				520
λō	1561	CTTGACGG	TCGCCCCCTCTCCAC	CATCCAGCAGTACTC	CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG	1620
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රු සි	1681	TATAACAC	CACTGCTAGCGACCA	ACTGCTTGTCGAGAA 	TATAACACCACTGCTAGCCAACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT 	1740 590
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è e	1861	CATACTTT	TGATGATTTCTGCCC.	AGAGTGCCGCCCCCT	CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC	1920
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දු පු	1921	CAGTCTAC	TGTCGCTGAGCTTCA	SCGCCTTAAGATGAA                \argLeuLysMetLy	CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 	1980 660
RESULT 2 B44212 Structural C; Species: C; Date: 17: C; Accession R; Huang, C; Accession R; Huang, A; Title: M A; Reficues A; Reficues A; Residues A; Cross-re C; Superfam C; Superfam C; Reywords F; 23-6590m F; 23-6590m F; 23-6590m F; 23-6590m	tral protects: hepen 17-Feb-1	ttein 2 pratitis E patitis E 44212 #84212 #84212 mular clor maber: A44 mular clor mater: A44 mular clor mater: A44 mular clor mater: A44 mular clor e: genomic e 55 club mater: A44 mular clor e: signal sign	RESULT 2 B44212 Structural protein 2 precursor - hepatitis B C; Species: hepatitis E virus C; Date: 17-Feb-1994 #sequence_revision 17-Feb C; Accession: B44212 C; Accession: B44212 A; Fitale: Molecular cloning and sequencing of A; Reference number: A44212; MUID:93079857; PW A; Accession: B44212 A; Molecule type: genomic RNA A; Accession: B4212 A; Molecule type: genomic RNA A; Accession: B4212 C; Superfamily: hepatitis E virus structural p C; Superfamily: hepatitis E virus structural p C; Reywords: structural protein F; 1-22/Domain: signal sequence #status predic F; 23-659/Product: structural protein 2 #status Alignment Scores: C: Reywords: Sores: C: C	itis E virus (st 1 17-Feb-1994 #te J.; Yun, K.Y.; E ing of the Mexic 8857; PMID:144891 10017; PIDN:AAA45 ttural protein 2 spredicted <sig> #status predict</sig>		W.; Tam, A.W. s E virus (HE
Score:				Matches:	120	

Qy         122 TCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	RESULT 4 C44212 structural protein 1 - hepatitis E virus (strain Mexico) C;Species: hepatitis E virus C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999 C;Accession: C44212 R;Huangy 191, 550-558, 1992 A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE A;Reference number: A44212; MUID: 93079857; PMID: 1448913 A;Accession: C44212 A;Molecule type: genomic RNA A;Residues: 1-123 <-HUA> A;Cross-references: GB:MT4506; NID:g330017; PIDN:AAA45731.1; PID:g330019 C;Superfamily: hepatitis E virus structural protein 1 C;Keywords: structural protein	Alignment Scores: Pred. No.: Score: Score: Score: Store: S		RESULT 5 B40236 B40236 Structural protein 1 - hepatitis E virus (strain Indian) C; Species: hepatitis E virus C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999 C; Accession: B40236 R; Ray, R.; Jameel, S.; Manivel, V.; Ray, R. Virology 189, 335-3362, 1992 A; Title: Indian hepatitis E virus shows a major deletion in the small open reading frame A; Reference number: A40236; MUID:92295577; PMID:1534953 A; Accession: B40236 A; Molecule type: genomic RNA A; Molecule type: genomic RNA A; Residues: 1-41 < RAY> C; Superfamily: hepatitis E virus structural protein 1
Descent Similarity:   100.00\$   Conservative: 0	204 GlyTyrAlaileSerileSerPheTrpProdInThrThrThrThrProThrSerValAsp 670 ATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAG 224 MetAsnSerIleThrSerThrAspValArglleLeuValGlnProGlyIleAlaSerGlu 730 CTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACC [	VHWHILE VITABLE VITABL	Virology 189, 359-362, 1992  Virology 189, 359-362, 1992  A; Title: Indian hepatitis E virus shows a major deletion in the small open reading frame A; Reference number: A40236; MUID:92295577; PMID:1534953  A; Recession: A40236  A; Recession: A40236  A; Residues: 1-57, Pr. 59-102, Pr. 104-123 «RAY> C; Superfamily: hepatitis E virus structural protein 1 C; Keywords: structural protein Alignment Scores: 1.85e-98  Length: 123 Pred. No.: 1.85e-98  Length: 109  Ratches: 109  Percent Similarity: 100.00% Conservative: 0	100.00\$   Mismatches:   16.52\$   Indels:   Gaps:

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Unknown protein, 73054-77165 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hunge, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.K.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Hitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H96635
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Date: 01-Bec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83928
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Molecule type: DNA
A;Residues: 1-1091 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05949.1; GSPDB:GN00
A;Experimental source: strain C-125
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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Conservative:
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A;Molecule type: DNA
A;Residues: 1-840 <STO>
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A,Gene: T7P1.16
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A;Description: Molecular phylogeny of a live-bearing fish genus Poecilia (Cyprinidontific A;Reference number: 217479
A;Accession: T12281
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ritheologis, A.; Beker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712
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C;Date: 23-Jul_1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002
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C;Genetics:
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C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
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A;Molecule type: DNA
A;Residues: 1-337 <STO>
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     C; Keywords: structural
                                                                                                                              Percent Similarity:
Best Local Similarity:
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R; Breden, F.; Ptace
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US-09-851-410A-6\_

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Alignment Scores: Pred. No.:

No.:

A; Gene: BH2230

protamine II - black rat snake (fragment)

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Pypothetical protein NMB0903 [imported] - Neiseeria meningitidis (strain MC58 serogroup C;Species: Neisseria maningitidis
C;Species: Neisseria maningitidis
C;Species: 13-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D3114

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Caradi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
                                                                                                                                                                                                                                                                                                                                                       A;Accession: D81144
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-97 <TET>
A;Cross-references: GB:AE002442; GB:AE002098; NID:g7226133; PIDN:AAF41311.1; PID:g722614
A;Experimental source: serogroup B, strain MC58
A;Gene: NMB0903
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Viscois: Herpetosiphon aurantiacus
C;Species: Herpetosiphon aurantiacus
C;Species: Herpetosiphon aurantiacus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Mar-2000
C;Accession: JT0593; S21948
R;Duesterhoeft, A.; Kroeger, M.
Gene 106, 87-92, 1991
A;Title: Cloning, sequence and characterization of m5C-methyltransferase-encoding gene, A;Reference number: JT0592; MUID:92039068; PMID:1937045
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A,Residues: 1-138 <DUE>
A,Cross-references: EMBL:X55141; NID:g48771; PIDN:CAA38940.1; PID:g48772
A,Experimental source: strain Hpa2
C,Superfamily: Herpetosiphon aurantiacus hypothetical 15K protein (hgiDIIM 3' region)
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64 ThrArgProGluValAlaSerSer
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C;Species: Herpetosiphon aurantiacus
C;Species: Herpetosiphon aurantiacus
C;Species: Harpetosiphon aurantiacus
C;Accession: 319708
R;Erdmann, D.; Duesterhoeft, A.; Kroeger, M.
R;Erdmann, D.; Duesterhoeft, A.; Kroeger, M.
A;Title: Cloning and molecular characterization of the HgiCI restriction/ modification
A;Reference number: S19706, MuID:92111503; PMID:1662609
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: H58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Title: Protamines of reptiles.
A;Reference number: A58208; WUID:96394458; PMID:8798564
                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Elaphe obsoleta quadrivittata
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 07-May-1999
C;Accession: H58208
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TCTGGCCGCCGTCGTGGGCGCGC 99 

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Percent Similarity: Best Local Similarity:

Query Match:

C; Superfamily: sperm histone A; Molecule type: protein A; Residues: 1-41 <HUN>

Alignment Scores:

Pred. No.:

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A;Status: preliminary

1.21%

827 ACAAGACCAGAGGTAGCCTCCTCC 804

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A; Molecule type: DNA A; Residues: 1-74 < KRO>

A; Cross-references:

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EXDN/Tolk family protein [imported] - Caulobacter crescentus
C.Species: Caulobacter Caulobacter C.Species: Caulobacter C.Species: Caulobacter C.Species: Caulobacter C.Species: Caulobacter C.Species: Caulobacter C.Species: Caulobacter 
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A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-166 cARN>
A;Cross-references: GB:AE001711; GB:AE000512; NID:g4980788; PIDN:AAD35380.1; PID:g498079
A;Experimental source: strain MSB8
hypothetical protein TM0292 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72394
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                          seo
                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Recession: D72394
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xylella fas xylella fas

O75173 P57972 Q9ph22 Q87f43 P30601

pasteurella

mus musculu rattus norv homo sapien

P53762 P41739

Sequence:

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Searched:

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homo sapien

Q13064 P18183

mus musculu

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sapien caenorhabdi streptomyce synechocyst rattus norv oryctolagus

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fuli-length viral genome.";
Virology 185:120-131(1991).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
HAAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92024067; PubMed=1926770;
Mam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURAL PROTEIN 2.
5832A013CCC4A61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Burma) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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ARNT RAT
                             MAN1 MOUSE
PTPA HUMAN
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XYLFA
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InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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CHAIN
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-MODEL=frame+ n2p.model -DEV=xlp
-G=Cgn2_1/USF70_spool_p/US609851410/runat_16082004_125716_9625/app_query.fasta_1.4238
-G=Cgn2_1/USF70_spool_p/US609851410/runat_16082004_125716_9625/app_query.fasta_1.4238
-D=SwissProt 42 -QFMM=fastan -SUFFIX=oli.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-USFRT=pt -DCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09851410_@CGN 1 1 43 @runat_16082004 125716_9625 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG SCORES=0 -WAXIT -DSPBALCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THERAD=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-DGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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                                                                                                                                               1 ATGCGCCCTCGGCCTATTTT......GTAAAACTCGGGAGTTGTAG 1983
                                                                           August 16, 2004, 13:36:13 ; Search time 18.2638 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                      protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                        US-09-851-410A-6 COPY 5147 7129
                                                                                                                                                                                                                                      141681 seqs, 52070155 residues
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Result Š.

961 321 1021 341	Oy 1081 GTGGGTGAGATGGGCGGGGATAGG 	381	401	CAGGAIAAGGGIATIGCAAIG GlnAspLysGlyIleAlaIIle	441	1381	1441 4 8 1	501	1561	1621	1681	1741	1801	1861	Oy 1921 CAGTCTACTGTCGCTGAGCTTCAGCG	RESULT 2 VST2 HEVDA  ID VST2 HEVPA STANDARD; PRT; AC P33426;
Alignment Scores:     Pred. No.:     Score:     Score:     Score:     Score:     Percent:     Score:     Percent:     Perc	TTTGTTGCTGCTCCTC	Qy 61 CCGCCCGGTCAGCCGTCGTCGTCGGCGCGCCACGCGCGCG	Qy         121 TTCTGGGGTGACCGGGTTGATTCTCAGCCTTCGCAATCCCCTATATTCATCCAACCAA	Oy 181 CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTCGACCTCGTGTTCGCCAACCCGC 240	Qy 241 CGACCACTCGGCTCGCCTGGCGTGACCAGGCCCCGCCGTTGCCTCACGTCGT 300	Qy 301 AGACCTACCACAGGGGCGCGCGCGCTAACCGCGGTCGCTCCGGCCCATGACCCCG 360	Qy 361 CCAGTGCCTGATGTCGACTCCCGGGGGCGATCTTGCGGCGGCGGTATAACCTATCAACA 420	Qy 421 TCTCCCCTTACCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCCTCTT 480	Qy         481 AGTCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540	Qy 541 AATTATGCCCAGTACCGGGTTGCCCGTGCCCCAATCCGTTACCGCCCGC	Qy 601 GCTGTCGGCGGTTACGCCATCTCCATCTCATCTGGCCACAGACCACCACCACCGGGG 660	Qy 661 TCCGTTGATATGAATACCATAGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720	Qy 721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCTACACTATCGTAACCAAGGCTGGCGCTCC 780	Qy 781 GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840	Qy 841 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 900  281 HisGlySerLeuValAsnSerTyrfhrAsnfhrProTyrfhrGlyAlaLeuGlyLeuLeu 300	901 GACTTTGCCCTTGAGTTTCGCAACCTTACCCCGGTAACACCAATACGCGGGTC 96 

EVPA STANDARD; PRT; 660 AA.	rz_HEVPA VST2_HEV P33476:	S OI
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. GTTAATGTTGCGACCGGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACA	150	ò
44] GACCASICCATTATAGCTCTTCGACTAGACTTTATATTTTCTGACTTGATGATTAGATTAGATTAGACTTGATGATGATGATGATGATGATGATGATGATGATGATGA	144. 48.	음 성
l PropheservalLeuargalaasnaspvalLeuTrpLeuserLeuThralaalaGluTyr 480	46.	QQ
81 CCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT	138:	ò
	44.	qq
21 CAGGATTATGATAACCAACAAGAAGATGGGCCGACGCCTTCTCCGGCCCCATCGCGC	132	ΟŻ
	42.	qq
61 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTATT	126	ò
	40:	Ωp
GITGLCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG	120:	ò
		qu
1 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC	114	ò
	36.	qq
1 GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT 1	108	ò
	34.	qq
CTCACCACCACGGCTGCTACCGGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1	102	QY
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61 TCCCGTTATTCCAGCACTGCTCGCCACGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 10	.96	ò

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GACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 1188
                                        GInProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGln
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                                                                                      GGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTT
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                     CAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAA
                                                                                                           GlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuVal
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                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=92115700; DubMed=1731327;

MEDLINE=92115700; DubMed=1731327;

Malik I.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,

Malik I.A., Igbal M., Purcell R.H.;

"Characterization of a prototype strain of hepatitis E virus.";

Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING

THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA

BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST2_HEVPA (1-660)
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STRUCTURAL PROTEIN 2.
9085BC53CF846FD3 CRC64;
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Matches:
Conservative:
Mismatches:
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Heparitis E virus (strain Pakistan) (HEV).
Viruses; SERNA positive-strand viruses, no DN
Heparitis B-like viruses.
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Signal.
SIGNAL 1 22
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Best Local Similarity:
Query Match:
DB:
                                                                                                                  NCBI TaxID=33774;
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660 A
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Pred. No.:
Score:
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                                           853 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTT
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                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Structural protein 2 (Fragment)
Vepatitis E virus (isolate Rhesus) (HEV)
Viruses; ssRNA positive-strand viruses, no DNA stage;
MCPATILIS E-like viruses.
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Matches:
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Uchida T., Suzuki K., Hayashi N., Iid
Wang C.-K., Shikata T., Ichikawa M.,
Win K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR004261; SP2.
Interpro; IPR008975; Viral_cap_coat.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=31766;
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DB:
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Virus Genes 7:95-109(1993).

Virus Genes 7:95-109(1993).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.

BY EFFECTIVELY NEUTRALIZING THE OFFICE OFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                   T., Ichikawa
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                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; ssNAA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata
Rikihisa T., Winn K.;
                                                                                                                                             660 AA
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Gaps:
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                          GCGGTTGCCGTTTTAGCCCCCCCACTCT
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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  790 TCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCA 849
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                                                                                                                         244 LeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Pakistan;
MEDLINE=92115700; PubMed=1731327;
Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
Malik I.A., Iqbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.",
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Burma;
MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Tam F.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Tam P.W. K.E., Reyes G.R.;
"Hepatitis E virus (HEW): molecular cloning and sequencing of the
full-length viral genome.";
Virology 185:120-131(1991).
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SEQUENCE 123 AA; 12676 MW; 8A5A798B1B74EDE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein I (ORF3).
Hepatitis E virus (strain Burma) (HEV), and
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
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                                                                                                                                          549
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                               1153 ACAGAATTGATTTCGTCGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC
1093 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93079857; PubMed=1448913; Huang C.C., Nguyen D., Rernadez J., Yun K.Y., Fry K.E., Bradley D.W., Tam A.W., Reyes G.R.; "Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E virus (HEV).";
Virology 191:550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST2_HEVME (1-659)
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CF75E75EFD8FBE2C CRC64;
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Viruses; BSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Interpro; IPR004261; SP2.
Interpro; IPR008975; Viral_cap_coat.
Pfam; PF03314; SP2; 1.
                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequ
01-FEB-1994 (Rel. 28, Last anno
Structural protein 2 precursor.
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70640 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31768;
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Q03500;
                                                                                                                                                              253
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DB:
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VST2_HEVME
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Virology 191:550-558(1992).
                                                                                                                                 Structural protein 1.
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                                                                                                              GACCACTCGGCTCCGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGTA 301
                                                                                                                            AspHisSerAlaProLeuGlyValThrArgProSerAlaProProLeuProHisValVal 114
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                                           74
                                                                              ValSerArgLeuAlaAlaValValGlyGlyAlaAlaAlaValProAlaValValSerGly
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                                                                  CCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCCC
35 ArgProValSerArgLeuAlaAlaValValGlyGlyAlaAlaAlaValProAlaValVal
                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GICAGCCGICTGGCCGCCGTCGTGGCGCGCGCAGCGGCGGTTCCGGCGGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST1_HEVMY (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D10330; BAA01173.1; -.
Interpro; IPR003384; HEV_ORF2.
Pfam; PF02444; HEV_ORF2; 1.
SEQUENCE 123 AA; 12751 MW; FB81143F0B31F8A4 CRC64;
                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1995 (Rel. 32, Last annotation update)
Structural protein 1 (ORF3).
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; SSRNA, positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Mismatches:
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Matches:
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Pred. No.:
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235
                                            92
  CCCCCGATGTCACCGCTGCGCCTGGACCTCGTGTTCGCCAAC
                             ProprometSerProLeuArgProGlyLeuAspLeuValPheAlaAsn
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                                                                                                                                                                                                                                                                                    Hepatitis E virus (strain Mexico) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=31768;
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                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
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Matches:
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DIR; G44212; C44212.
InterPro; IPR003384; HEV_ORF2.
Pfam; PF02444; HEV_ORF2; 1.
CPONTENCE 123 AA; 12714 MW;
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Theologis A., Ecker J. 1190712,

Theologis A., Ecker J. Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Nierman W.C., Osborne B.I.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Paid G., Peterson J., Pham P.K., Rizzo M., Kooney T., Rowley D.,

Sakano H., Zalzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                            Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=21125776; PubMed=11042177;
Burks E.A., Bezerra P.P., Le H., Gallie D.R., Browning K.S.;
Burks Initiation factor 3 subunit composition resembles mammalian initiation factor 3 and has a novel subunit.";
J. Biol. Chem. 276:2122-2131(2001).
translation initiation factor 3 subunit 3 (eIF-3 gamma)
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
            (eIF3 p38 subunit) (eIF3h).
TIF3H1 OR AT1G10840 OR T16B5.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:816-820(2000).
                                                                                                                                                SEQUENCE FROM N.A
                                                                                                              NCBI_TaxID=3702;
 Eukaryotic
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SEQUENCE FROM N.A.

C STRAIN=cv. Columbia;

MEDLINE=2954865; PubMed=14593172;

Yamada K. Lim J. Dale J.M., Chen H., Shinn P., Palm C.J.,

Yamada K. Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Karlin-Newmann G., Liu J. S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu J. S.X., Lam B., Sakano H., Wu T., Yu G.,

A Chan M., Tango C.C., Onodera C.S., Deng J.M., Akiyama K., Annari Y.,

A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hannen N.P.,

A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hannen N.P.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakim, Sakurai T.,

A Kamiya A., Meyers C., Nakajima M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Pheologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 302:842-846(2003).
-!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE P170 SUBUNIT OF
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-!- SUBUNIT: eIF-3 is composed of at least 12 different subunits.
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Alignment Scores:

EMBL; AF285833; AAG53614.1; -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Seems to be the binding site for several of the factinvolved in protein synthesis and appears to be essential for accurate translation (By similarity).
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-851-410A-6_COPY_5147_7129 (1-1983) x IF33_ARATH (1-337)
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SEQUENCE 121 AA; 12535 MW; 5AF9F83D2C94AC3E CRC64;
                                                                                                                                                                                                                                                                                                               V -> L (IN REF. 1).
F9965DA546AC977C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          337
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Mismatches:
Indels:
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solosomal protein L7/L12.
FPLL OR CPE2414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AA
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Matches:
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                                                                                    PIR; B86242; B86242.
InterPro; IPR003639; Pept M67 Mov34.
InterPro; IPR000555; Peptidase_M67.
Propom; PD363422; Mov34 1; 1.
SMART; SM00232; JAB MPN; 1.
Initiation factor; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 LeuLysAlaLeuLysLeuSerAspSer 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00368; -; 1.
InterPro; IPR008932; Ribos_L12/7_olig.
InterPro; IPR000206; Ribosomal_L12.
Pfam; PF00542; Ribosomal_L12; T.
Probom; PD001326; Ribosomal_L12; 1.
TIGRPAMS; TIGR00855; L12; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
AC007354; AAD31329.1; -. AY054641; AAK96832.1; -. AY081546; AAM10108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP003194; BAB82120.1; -.
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                                                                                                                                                                                                                                                                                                                                            337 AA;
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Q8XHR7;
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                                EMBL;
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SEQUENCE FROM N.A.
STRAIN=137c / CC-125;
 Thermotoga maritima.
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P12852
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                                                                                                                                                                                                                                                                                                                     MEDLINE=92039068; PubMed=1937045; Duesterhoeft A., Kroeger M., "Cloning, sequence and characterization of m5C-methyltransferase-encoding gene, hgiDIIM (GTCGAC), from Herpetosiphon giganteus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
3-isopropylamalate dehydratase small subunit 1 (EC 4.2.1.33)
[Isopropylamalate isomerase 1) (Alpha-IPM isomerase 1) (IPMI 1).
LEUDI OR TM0292.
                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 15-4 kDa protein in HgiDIIM 5'region (ORF15).
Herpetosiphon aurantiacus (Herpetosiphon giganteus).
Bacteria; Chloroflexi; Herpetosiphonales; Herpetosiphonaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-851-410A-6_COPY_5147_7129 (1-1983) x YD2M_HERAU (1-138)
                                                                              US-09-851-410A-6_COPY_5147_7129 (1-1983) x RL7_CLOPE (1-121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JT0593; JT0593.
Hypochetical protein; Restriction system; DNA-binding.
DNA BIND 17 38 H-T-H MOTIF (POTENTIAL).
SEQÜENCE 138 AA; 15396 MW; E9CC70A0E11785A2 CRC64;
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           Matches:
Conservative:
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Mismatches:
                                  Mismatches:
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Matches:
                                             Indels:
Gaps:
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                                                                                                                 ThrArgGlySerLeuLeuLeuSer 50
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                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                  Best Local Similarity:
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Best Local Similarity:
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                       Percent Similarity:
                                                                                                                                                                                                                                                                Herpetosiphon.
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                                             Query Match:
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 Pred. No.:
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                                                                                                    STRAIN=MSB8 / DSM 3109 / ATCC 43589;
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last amontation update)
Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Leucine biosynthesis; second step. SUBUNIT: Heterodimer of leuC and leuD (By similarity). SIMILARITY: Belongs to the leuD family. LeuD 2 subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0 = 2-
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InterPro, IPR000573; Aconitase_C.
Pfam, PF00694; Aconitase_C; 1.
Leucine biosynthesis; Lyses; Complete proteome.
SEQUENCE 166 AA; 18734 MW; D8ACF340205111A4 CRC64;
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Mayfield S.D., Schirmer-Rahire G., Frank H., Zuber H., Rochaix J.-D.; Analysis of the genes of the OBE1 and OBE3 proteins of the photosystem II complex of Chlamydomonas reinhardtii."; Plant Mol. Biol. 12:683-693 (1989).

-!- SUBCELDULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.

-!- SIMILARITY: Belongs to the psbQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITRE-96376499; PubMed-8781179;
Choi G., Przybylska M., Straus D.;
Three abundant germ line-specific transcripts in Volvox carteri
encode photosynthetic proteins.";
Curr. Genet. 30:347-355 (1996).
-!- SUBCELLUIAR LOCATION: Chloroplast thylakoid membrane; associated
with the photosystem II complex.
-!- SIMILARITY: Belongs to the psbQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3).
PSBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Volvocaceae, Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST.

OXYGEN-EVOLVING ENHANCER PROTEIN 3.

8CCF077334CF79D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-199)
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Mismatches:
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Matches:
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STRAIN=f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13832; CAA32061.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF05757; PsbQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S05509; S05509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thylakoid; Membrane
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PSBQ VOLCAL
DSBQ AC Q4164
DT 16-0C
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         임
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC 33913 / NCPEB 528;

STRAIN-ATCC 33913 / NCPEB 528;

MEDILINE-22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.E.B.,

Anderotte G., Cannavan F., Cardozo J., Chambergo F. Ciapina L.P.,

Ramarotte G., Cannavan F., Cardozo J.C., Farro M.I.T.,

Rario J.B., Ferrach A.D.S., Perrelia R.C.C., Ferrol M.I.T.,

Rormighieri B.F., Franco M.C., Greggio C.C., Ferrol M.I.T.,

Locall E.C., Machado M.A., Madeira A.M.B.N., Matrinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Matrinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.P.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Schubal J.C., Kitajima J.P.,

R. "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Plays a critical role in the incorporation of lipoproteins in the outer membrane after they are released by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lola protein (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                 CHLOROPLAST (POTENTIAL).

OXYGEN-EVOLVING ENHANCER PROTEIN 3.

3103DDFC84CC3180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris (pv. campestris).Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                            Pfam; PF05757; PsbQ; 1.
TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-851-410A-6_COPY_5147_7129 (1-1983) x PSBQ_VOLCA (1-202)
                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Outer-membrane lipoprotein lolB precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA.
                                                                                                                                                                                                                                                                                                Matches:
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-!- SIMILARITY: Belongs to the lolB family.
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U22330; AAB40980.1; -.
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8.00
100.00%
100.00%
1.21%
                 PIR; S72224; S72224.
InterPro; IPR008797; PsbQ.
InterPro; IPR006311; Tat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                   54
                                                                                                                                              Thylakoid, Membrane.
IRANSIT
                                                                                                                                                                                     CHAIN 55
SEQUENCE 202 AA;
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Query Match:
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Q8PC65;
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US-09-851-410A-6_COPY_5147_7129 (1-1983) x LOLB_XANCP (1-218)
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                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                    50.6
8.00
100.00%
100.00%
1.23%
                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                Alignment Scores:
Pred. No.:
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Search completed: August 16, 2004, 13:48:43 Job time : 28.2638 secs

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MEDLINE-20271579; PubMed=10813471;
MEDLINE-20271579; PubMed=10813471;
Wan Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.,
"Phylogenetically distinct hepatitis E viruses in Pakistan.";
Am. J. Trop. Med. Hyg. 62:187-189(2000).
EMBL; AF185822; AAG16766.1;
GO; GO:0005198; F:structural molecule activity; IEA.
                     Q9wjz5
Q9wjz5
Q9wjz5
Q9wjz1
Q69411
Q69411
Q69411
Q9y810
Q9y810
Q9y811
Q9
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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Last annotation update)
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091855
Q9YWL0
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Q81860
Q81878
Q9YPB1
                                 Q9WJZ5
Q81871
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039947
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Q81861
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O56049
Q9WI48
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QBB6I9
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Q91169
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InterPro, IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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                                          (TrEMBLrel. 16, (TrEMBLrel. 16,
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Hepatitis E virus.
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Q9E8G5
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Q9E8G5
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12890.708 Million cell updates/sec
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                                                                                                                                   1 ATGCGCCCTCGGCCTATTT.....GTAAAACTCGGGAGTTGTAG 1983
                                                                    August 16, 2004, 13:39:23 ; Search time 97.0734 Seconds
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                               protein search, using frame_plus_n2p model
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SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;	Alignment Scores:  Pred. No.: Score: Score: 456.00 Matches: 556 Secret: 5imilarity: 99.82\$ Mismatches: 1 Query Match: 12.09\$ Indels: 0 DB:	US-09-851-410A-6_COPY_5147_7129 (1-1983) x Q9E8G5 (1-660)	Oy 310 ACAGCTGGGGCGCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCT 369 	Qy 370 GAIGICGACTCCCGCGGCGCCATCTTGCGCCGGCAGIATAACCTAICAACAICTCCCCTT 429	Oy 430 ACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCTCTTAGTCCGCTT 489	Oy 490 TTACCCCTTCAGGACGGCACCAATACCCATATAANGGCCACGGAAGCTTCTAATTATGCC 549	Qy 550 CAGTACCGGGTTGCCCGTGCCAATCCGTTACCGCCGCTGGTCCCCAATGCTGTCGGC 609	Qy 610 GGTTACGCCATCTCCATCTCCATTCTGGCCACAGCCACCACCACCGCGGTCCGTTGAT 669	Qy 670 ATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGCGTAGCCTCTCAG 729	Oy 730 CTTGTGATCCCAAGTGGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGAACC 789	Oy 790 TCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCA 849	Qy 850 CTCGTAAATTCCTATACTAATACACCCTATACCGGGCCCCTCGGGCTGTTGGACTTTGCC 909  Db 284 ProvalAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 303	Qy 910 CTTGAGCTTGAGATTCGCAACCTTACCCCGGTAACACCAATACGCGGGTCTCCCGTTAT 969	970	GTGAG	0 4	1150 CCGACAGAATTGATCGCCGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 1	

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TACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGG 1728
      CGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCA
                                   TACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGGTTGTATACATCTGTA
                                              397 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal
                                                                        GAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCT
                                                                                    GCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCCAGTTTATGTTTCTGAC
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MEDLINE=S9171571; PubMed=7871758;
MEDLINE=9517571; PubMed=7871758;
Thin S., Pircell R.H., Emerson S.U.;
"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
Virus Genes 9:23-32(1994).
EMBL; L25547; AAA65490.1; -.
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the EMBL/GenBank/DDBJ databases
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Viruses; ssRNA positive-strand viruses, no DNA
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Yin S.R., Purcell R.H.,
Submitted (MAR-1996) to
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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403.00
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99.80%
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                                                                                      Percent Similarity:
                                                         Alignment Scores:
Pred. No.:
Score:
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                                   AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT
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STRAIN=MOTOCCO;
GTRAIN=MOTOCCO;
"Identification of the 5' Capped and 3' Complete Terminal the Hepatitis E virus Isolated From Morocco.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065061; AAD10627.1;
EMBL; AY230202; AAO72992.1; -.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein 2 (Structural viral protein).
Hepatitis E virus.
Hepatitis E virus.
Hepatitis E-like viruses.
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STRAIN=HBV-Morocco;
STRAIN=B9107414; PubMed=9892396;
Meng J., Cong M., Dai X., Fillot Khudyakov Y.E.;
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Matches:
Conservative:
Mismatches:
Indels:
       GO, GO:0005198; F:structural molecule activity; InterPro; IPR004251; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PR03014; SP2; 1, SP2; SEQUENCE 660 AA; 70979 MW; DC68116DCD639175
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TCTGTGACCTTGGTTAATGTTGCGACCGGCGCAGGCCGTTGCCCGGTCGCTCGATTGG 1548
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   GluAsnAlaGlnGlnAspLysGlylleAlaIleProHisAspleaglyGluSer
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                                                             GCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCCAGTTTATGTTTCTGAC
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 24, Last sequence update)
01-UNO-2003 (TrEMBLrel. 24, Last annotation update)
Structural protein 2 (Fragment).
Viruses; SSRNA positive-strand viruses, no DNA stags
Hepatitis B-like viruses.
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GO; GO:0005198; F:structural molecule .
InterPro; IPR004261; SP2.
Pfar:PPro; IPR008975; Viral_cap_coat.
Pfar: PPro314; SP2; 1.
SEQUENCE 660 AA; 70943 MW; 9719D30
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MEDLINE=92271462; PubMed=1589964;
Fry K.B., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
Fry K.B., Tam A.W., Swith M.W., Yun K.Y., Purdy M.A., McCaustland K.A.,
Bradley D.W., Reldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A.,
Bradley D.W., Reyes G.R.,
"Hepatitis E virus (HEV): Strain variation in the nonstructural gene
region encoding consensus motifs for an RNA-dependent RNA polymerase
and an ATP/GTP binding site.";
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Xinjiang epidemic (1986-1988) of China.";
Nucleic Acids Res. 20:3512-3512(1992).
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MEDLINE-92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92115700; PubMed=1731327;
Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters Malik I.A., Idbal M., Purcell R.H., "Characterization of a prototype strain of hepatitis E virus. Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
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Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno I
"Hepatitis E virus: cDNA cloning and expression.";
Microbiol. Immunol. 36:67-79(1992).
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Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T.,
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Virology 185:120-131(1991).
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                     Van Cuyck-Gandre H., Clements N.J., Zhang H.Y., Caudill J.C., Cohen S.G., Coursaget P., Buisson Y., Warren R.L., Longer C.F., "Partial Sequence of HEV Isolates from North Africa and Pakistan: Comparison with Known HEV Sequences.", Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
           Caudill J.C.,
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InterPro: IPR04261; SP2.
Pfam; PF03014; SP2; 1.
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STRAIN=TK15/92;
MEDLINE=9049628; PubMed=9833882;
Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
"Heparitis E virus: complete genome sequence and phylogenetic of a Nepali isolate.";
Virus Res. 57:21-26(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gouvea V.; MAR-1998) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-1998) to the EMBL, AF051830; AAC97188.1; -- GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR004261; SP2. InterPro; IPR008975; Viral_cap_coat.
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Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no
Hepatitis E-like viruses.
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           | EDUCENCE FROM N.A. MEDGLUSS. | EDUCE FROM N.A. MEDGLUSS. | EDUCENCE FROM N.A. MCGaustland K.A., Margolis H.S., Bradley D.W.; "The sequence of hepatitis E virus isolated directly from a single source during an outbreak in China."; Virus Fes. 28:233-247(193). | EMBL, LO8816; AAAO3191.1; -. GO; 000198; F:structural molecule activity; IEA. InterPro; IPR004261, SP2. | InterPro; IPR04261, SP2. | InterPro; IPR04261
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                                    ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC
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SEQUENCE FROM N.A.
MEDLINE=22072932; PubMed=12076829;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
"Reevaluation of a North India isolate of hepatitis E virus based on the full-length genomic sequence obtained following long RT-PCR.";
Virus Res. 86:53-58(2002).
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Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR4554918; AAM66330.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; Viral_cap_coat.
SEQUENCE 659 AA; 70842 MW; ABCC177EBE6012C8 CRC64;
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Viruses; ssRNA positive-strand viruses,
Hepatitis E-like viruses.
VCBI_TAXID=12461;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ORF1, ORF2 & ORF3.
Hepatitis E virus.
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InterPro; IPR008975; Viral_cap_coat.
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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SEQUENCE 660 AA; 70960 MW;
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                       GATITCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTC
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"Sequence analysis of full length HEV clones derived directly human liver in fulminant hepatitis E.";
III) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
VIRAL HEPATITIS AND LIVER DISBASE, pp.313-316,
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Harrison T.J.;
Submitted (JTN-1996) to the EMBL/GenBank/DDBJ daraba
BLBL; X99292; CAA66937.1; -
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Hepatitis E-like viruses.
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01-JAN-1998 (TrEMBLrel. 05, La
01-OCT-2003 (TrEMBLrel. 25, La
Structural protein.
Hepatitis E virus.
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"Phylogenetic analysis of heatitis E virus isolates from Egypt.";
J. Med. Virol. 57:68-74(1999).

BMBL; AF051551; AAC35761.1;
GO; GO:0005199; Ferructural molecule activity; IEA.

InterPro; IPR004261; SP2.

InterPro; IPR008975; Viral_cap_coat.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last annotation update)
Structural protein.
Hepatitis E virus.
Viruses, SRRM positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NISI_TAXID=12461;
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STRAIN=93-EGYPt;
MEDLINE=99105430; PubMed=9890424;
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MEDLINE=99013657; PubMed=9797311;
Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;
Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;
"Characterization of a strain of infectious hepatitis E virus isolated from sewage in a narea where hepatitis E is not endemic.";
Appl. Environ. Microbiol. 64:4485-4488(1998).
EMBL, AF058684; AAC7780801;
EMBL, AF058684; P.Structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR0084251; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein (Fragment).
Hepatitis E virus.
Viruses, SRRM positive-strand viruses, no DNA stage
Hepatitis E-like viruses.
NCH_TAXID=12461;
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                                                                         STRAIN=94 Egypt;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
Varaeve S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis E virus isolates from Egypt."
"Phylogenetic analysis of hepatitis E virus isolates from Egypt."
"Med. Virol. 57:68-74(1999).
"InterPro; IPRO04261; SP2.
InterPro; IPRO09975; Viral_cap_coat.
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                  DNA stage;
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            Viruses, ssRNA positive-strand viruses, Hepatitis E-like viruses.
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091856;
01-NOV-1998 (TrEMBLrel. 08, Ca
01-NOV-1998 (TrEMBLrel. 08, La
01-OCT-2003 (TrEMBLrel. 25, La
Structural protein.
                                                 3.46e-237
247.00
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               AA;
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                                 TTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAACACCCACTGCTAGC
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Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03014; SP2; 1. _ _ _ SRQUENCE 660 Aa; 70937 MW; 5412313F1A2EF4A9 CRC64.
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Hepatitis B-like viruses.
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GO, GO:005198; F: Ristructural molecule activity;
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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STRAIN-BURNAED:1-3;
MEDLINE-92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of the
                                                                                                                                                                                                                                                                                                               "Sequence comparison of the capsid region of Hepatitis E viruses isolated from Myanmar and China.";
Microbiol. Immunol. 36:615-621(1992).
EWEL; D1033; BAA01179.1; -
EWEL; D1033; BAA01179.1; -
InterPro; IPRO04261; SP2.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRXIN=BurmaEpi-1-3;
MEDLINE=92396046; PubMed=1387921;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Zhuang H.,
Win K.M.;
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                                                                           01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Structural protein (Fragment).
Hepatitis E virus.
Hepatitis EstNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Virology 185:120-131(1991)
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Pfam; PF03014; SP2; 1.
                                PRELIMINARY;
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Best Local Similarity:
                                                                                                                                                            SEQUENCE FROM N.A.
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APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 505 Penobscot Drive CITY: Redwood City
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Matches:
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     TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                     (1-1983) x US-08-259-148A-19 (1-660)
            Conservative:
Mismatches:
 Matches:
                                          Indels:
660.00
100.00%
100.00%
100.00%
                                                                                          US-09-851-410A-6_COPY_5147_7129
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                 Krawczynski, Krzysztof Z.
Yarbough, Patrice D.
VENTION: Hepatitis E Virus Vaccine and Method
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  APPLICANT: Yalvon APPLICANT: TILLE OF INVENTION: Hepon NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSEE: Dehlinger & Associates Timer: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, BURMA, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 39,615
REPERBNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURKENY APPLICATION DAILS.
CURKENY APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
PILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTORNEY AGENT INFORMATION:
AMAME: SHOILT NUMBER: US 208,997
FILING DATE: 17-JUN-1988
                                                                                                              Sequence 19, Application US/08259148A Patent No. 5741490 GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: Reyes, Gregory R. APPLICANT: Bradley, Daniel W. APPLICANT: Twu, Jr.Shin APPLICANT: Purdy, Michael A. APPLICANT: Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORF
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MEDIUM TYPE: Floppy disk
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amino acid
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NO
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HYPOTHETICAL:
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                                                                                       RESULT 2
US-08-259-148A-19
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Length:

Alignment Scores: Pred. No.:

320

Virus Vaccine and Method

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COMPOUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
                                                                                        STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
STATE: CA
CUNTRY: USA
      APPLICANT: Bradley, Daniel W. APPLICANT: Twu, Tr-Shin APPLICANT: Purdy, Michael A. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Krawczynski, Krzysztof Z. TITLE OP INVENTION: Hepatitis E Viru NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                 94306
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Length:
Matches:
Conservative:
Mismatches:
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Gaps:
CLASSIFICATION: 424

REIGN APPLICATION 1 424

PRIOR APPLICATION NUMBER: US 870,985

FILING DATE: 20-APRIL-1992

REIGN APPLICATION DATA:

APPLICATION NUMBER: US 822,335

FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

RAPPLICATION NUMBER: US 420,921

FILING DATE: 13-OCYOBER-1989

PRIOR APPLICATION NUMBER: US 367,486

FILING DATE: 16-JUNE-1989

PRIOR APPLICATION NUMBER: US 336,672

RILING DATE: 11-APRIL-1989

PRIOR APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

PRIOR APPLICATION NUMBER: US 208,997

FILING DATE: 17-JUNE-1988

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORF 2,
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amino acid
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Best Local Similarity:
Query Match:
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US-09-851-410A-6\_COPY\_5147\_7129 (1-1983) x US-08-484-054-19 (1-660)

RESULT 3
US-08-484-054-19
'Sequence 19, Application US/08484054
'Patent No. 5770689
'GENERAL INFORMATION:

APPLICANT: Reyes, Gregory R.

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                                                    81 ArgProLeuGlySerAlaTrpArgAspGlnAlaGlnArgProAlaValAlaSerArgArg
                                                                                                           121 ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr
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                                                                                            AGACCTACCACAGCTGGGGCCGCCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCG
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                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNIE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 189080
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APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-CATOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
PRIOR DATE: 16-UUNE-1989
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INDIVIDUAL ISOLATE:
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Palo Alto
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Best Local Similarity:
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Pred. No.:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                              NAME: Sholtz, Charles K.
RECISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0183.22
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNW-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                           APPLICATION NUMBER: US 07/505,888 FILING DATE: 05-APR-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/420,921 FILING DATE: 13-OCT-1989
                                                                                                                                                                                                      APPLICATION NUMBER: US 07/367,486 FILING DATE: 16-JUN-1989
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amino acid
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                          Enterically Transmitted
6120988-B Hepatitis Viral Agent
                                                            1741 ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08478507

Sequence 8, Application US/08478507

Patent No. 612098

GENERAL INPORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Tandley, Daniel W
APPLICANT: Tandley, Daniel W
APPLICANT: Tan, Albert
APPLICANT: Tan, Albert
ITLE OF INVENTION: No. 6120988-A/No. 612098

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-08-478-507-8
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                                                                                                     (1-1983) x US-08-542-634-13 (1-660)
                E Virus (Burma strain)
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Matches:
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  HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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APPLICANT: Yarbough, Patrice O
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Bradley, Daniel W
APPLICANT: Taw, Albert
APPLICANT: Taw, Albert
APPLICANT: Pry, Kirk E
TITLE OF INVENTION: No. 6229005-B Hepatitis Viral Agent
TITLE OF INVENTION: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
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Matches:
Conservative:
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REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
TELEFAX: (650) 324-0960
                                                       Sequence 8, Application US/09128275A Patent No. 6229005
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORF-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DG/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
FILING DATE:
FLING APPLICATION PATA:
APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTOMEX/AGENT INFORMATION:
ATTOMEX/AGENT INFORMATION:
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Conservative:
Mismatches:
                                                                                          Desjardins, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G32P5
TELECOMMUNICATION INPORMATION:
TELEPAC: (415)369-9500
TELEFAC: (415)368-0709
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE DADRESS: 24
CORRESPONDENCE ADDRESS:
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: US
ZIP: 94
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Best Local Similarity: 100.00%
Query Match: 100.00%
DB:
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amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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APPLICANT: Fuerst, Thomas
APPLICANT: McAtee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Zhang, Yifan
IIILE OF INVENTION: Hepatitis E Virus Antigens and Methods
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481 AspGlnSerThrTyTGlySerSerThrGlyProValTyTalSerAspSerValThrLeu 500  1501 UTAATGTTGCGACCGGGGCGCTGCCGGTCGTCGATGGACAAGGTCAAA  1501 UTAATGTTGCGACCGCGCGGGCGTCGCCGGTCGTTGATGACAAGGTCAAA  1501 UTAATGTTGCGACCGCGCGCGGGCCGTCGCTGGTCGTTGTTGTCTGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	APPLICANT: Tam, Albert APPLICANT: Tam, Albert APPLICANT: Fry, Kirk R  TITLE OF INVENTION: No. 6379891-B Hepatitis Viral Agent ITLE OF INVENTION: No. 6379891-B Hepatitis Viral Agent NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: Defilinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STRATE: CA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: IBM FC compatible OPERATING SYSTEM: PC-DSO/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 COMPUTER: BAPELICATION DATA: APPLICATION NUMBER: US/09/553,427 FILING DATE: 07-UN-1995 FILING DATE: 25-ULL-1994 PRICATION NUMBER: US 08/279,823 FILING DATE: 07-UN-1994 PRICATION NUMBER: US 07/681,078 FILING DATE: 05-APR-1991 PRICATATION NUMBER: US 07/681,078 FILING DATE: 05-APR-1991
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Matches:
Conservative:
Mismatches:
Indels:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles R.
REGISTRATION NUMBER: 4600-0183.22
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 4600-0183.22
TELERDHONE: (650) 324-0880
TELERDHONE: (650) 324-0880
INFORMATION CONTRACTORY
                                                                                                                                                                                                                                                                                                    0
660.00
100.00%
100.00%
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-553-427-8
                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                  NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCET DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER: 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-UUNBER: US 208,997
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Best Local Similarity:
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                                           441 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 460
                                                                                                               561 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 580
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                    CAGGATTATGATAACCAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
                                                                                                                                                                                   501 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/07870985A
Patent No. 6455492
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Paraley, Daniel W.
APPLICANT: Purdy, Michael A.
APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
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CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-07-870-985A-19
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DUAL ISOLATE: ORF-2	0 Length: 660 660.00 Marches: 660 100.00\$ Conservative: 0 100.00\$ Mismatches: 0 100.00\$ Indels: 0 50.00\$ Gaps: 0	6_COPr_5147_7129 (1-1983) x PCT-US95-13703-13 (1-660) TGGGCCCTGGGCTATTTTGTTGCTGCTCCTCATGTTTTTGCTATGCTGCCGGCCA 60	3TGGT       1yG1y	TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	CCTTCGCCCCCGATGTCACCGCTGCGGCCCGGACCTGGACCTCGTTTCGCCAACCCGCC 240	CGACCACTCGGCTTCGCGTGACCAGGCCCAGCGCCCGCGGTTGCCTCACGTGG 300 	AGACCTACCACAGCTGGGGCCGCGCTGACCGCGCTCGCTC	CAGTGCCTGATGTCGACTCCCGGGGGCGCCATCTTGCGCGGGGGTATAACCTATCAACA 420	CTCTT 	CTTCT 	CAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC	GCTGTCGGCGGTTACGCCATCTCCATCTCTGGCCACAGACCACCACCACGGCG 660	SCATA	78	1 00 0	CGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 9

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ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713
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                                                      GTTCGTATTTTAGTCCAGCCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA
                                                                                                                                                CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGGTGGCTGAGGAGGAGGCT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: FEBRENCE/DOCKET NUMBER: 4600-0293.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
TELEPHONE: (415) 324-0960
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                       APPLICANT: Fuerst, Thomas R.
APPLICANT: Modtee, C. Patrick
APPLICANT: Varbough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                               3: Dehlinger & Associates 350 Cambridge Ave., Suite
                                                                                                                                                                                                          ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                 Sequence 15, Application US/08542634
Patent No. 6214970
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 549 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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549.00
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100.00%
83.18%
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                                                                                                                                                            STREET: 350 Cambo
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                            GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                  ADDRESSEE:
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Pred. No.:
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US-08-542-634-15
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                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis E virus (Burma
r62kDa, FIGURE 4
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 anino acids
TYPE: amino acid
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Matches:
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100.00%
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83.18%
                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                             single
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
PCT-US95-13703-15
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GITIATGITICIGACTCIGIGACCTTGGITAATGITGCGACCGGCGCGCAGCCGTTGCC
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: PCT/US95/13703
FILING DATE:
CLASSIFICATION:
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GENERAL INFORMATION:
APPLICANT:
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ZIP: 94306-0850
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Search completed: August 16, 2004, 13:59:39 Job time : 57.0151 secs Hank Sheet

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Scoring table:

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Title: Perfect score:

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Sequence 11, Appl
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Sequence 92, Appl
Sequence 51, Appl
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Zhang, Yifan
TITLE OF INVENTION: HEPPATITIS E VIRUS ANTIGENS AND USES THEREFOR
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COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                               US-10-165-868-17
US-10-381-770-1
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ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fuerst, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice (
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RESULT 1
US-09-769-066-13
 Command line parameters:
-MODEL=frame+ n2p.model -DEV=x1p
-MODEL=frame+ n2p.model -DEV=x1p
-Q=/CgnZ 1/USFTO_spool p/US09851410/runat_16082004_125719_9771/app_query.fasta_1.4238
-Q=/CgnZ 1/USFTO_spool p/US09851410/runat_16082004_125719_9771/app_query.fasta_1.4238
-DE-Published Applications AA -OFMT=fastan -SUFFIX=oli.rapb -MINMATCH=0.1
-LOOPCL=0 -LOÖPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=oligo
-MATRIX=0-1000 - UST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09851410 @CGN 1 1_27 @runat_16082004_125719_9771
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY /NEG SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=12 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=6 -XGAPEXT=60
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                 GenCore version 5.1.6
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                                                                                                                                                                                                           strain)
                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                           (Burma
                                                                                 NAME: FADIAIN, GATY R.

REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-0an-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           Virus
                                                                                                                                                                                                                                                                                 NO: 13:
                                                                                                                                                                                                           ω
                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1
                                                                                                                                                                                                          STRANDEDNESS: Hepatitis ORF-2
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
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660.00
100.00%
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                            US-09-769-066-13
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Query Match:
DB:
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Matches:
Conservative:
Mismatches:
Indels:
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В
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
SEQUENCE TYPE: protein
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660.00
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
No. US20030124510A1-A/No. US20030124510A1-B Hepatitis Viral
                                                                                                                                                                                                                                                                                            1980
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LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn
                                                   ATTICCACTIACACCACTAGCCTGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
                                                                                                                    LeualaProHisSerAlaLeualaLeuGluaspThrLeuaspTyrProAlaArgAla
                                                                                                                                                                                                                                CATACTTTTGATGATTTCTGCCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC
                                                                                                                                                                                                                                                             HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe
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                                  TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,410
FILING DATE: 07-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/128,275
FILING DATE: cUnknown>
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: US 07/420,921
FILING DATE: 16-UN-1989
APPLICATION NUMBER: US 07/30,486
FILING DATE: 16-UN-1989
APPLICATION NUMBER: US 07/30,7486
FILING DATE: 11-APR-1989
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FILING DATE: 17-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reyes, Gregory R
Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof
Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09851410 Publication No. US20030124510A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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COUNTRY: U
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US-09-851-410-8
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CAGTCTACTGTCGCTCAGCTTCAGCGCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980
                              641 GlnSerThrValAlaGluLeuGlnArgLeuLySMetLysValGlyLysThrArgGluLeu 660
                                                                                                                                                                                                                                        Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRNIT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
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Matches:
Conservative:
Mismatches:
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ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APPLI-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APPLI-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
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NO: 19:
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APPLICATION UNDBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
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                                                                                RESULT. 5
US-10-165-868-19
; Sequence 19, Application US/10165868
; Publication No. US20030143241A1
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; Bradley, Daniel W.
; Twu, Jr-Shin
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SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                           Purdy, Michael A.
Tam, Albert W.
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            STATE: CA
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Best Local Similarity:
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    E VIRUS ANTIGENS AND USES THEREFOR
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                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Hepatitis B virus (Burma strain) r62kDa, FIGURE 4
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Matches:
Conservative:
Mismatches:
Indels:
                                                              250
                                                                                                                                                                                                                                                                                                                                 NAME: Fabian, Gary R.
REGISTRATION WINBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: HEPATITIS E VIRUS ANT.
NUMBER OF ENQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 25:
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                 NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
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MOLECULE TYPE: protein

HYPOTHETICAL: NO

CHIGINAL SURCE:

SEQUENCE DESCRIPTION: SEQ ID

US-09-769-066-15
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SEQUENCE CHARACTERISTICS:
                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
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US-10-257-044-1
                                                                1893
                                                                                                                    CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953
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                                                                GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTTCTGCCCAGAGTGCCGC
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Publication No. US20030220475A1
Publication No. US20030220475A1
APPLICANT: INFORMATION:
APPLICANT: Hegresented by the Secretary, Department of Health and APPLICANT: Human Services, Centers for Disease Control and Prevention APPLICANT: YURI B. KHUYAKOV
APPLICANT: YURI B. KHUYAKOV
APPLICANT: JIHONG MENG
                                                                                                                                                                                                                                                                                                                                                                              HEV POLYPEPTIDES (HEV)
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Mismatches:
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CURRENT APPLICATION NUMBER: US/10/257,044
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,380
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 660
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Matches:
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ORGANISM: Artificial Sequence
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US-10-257-044-1
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                                                                                                                                                 E virus (Burma strain)
                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                 REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDEDNESS: Hepatitis E virus
TOPOLOGY: linear
                                                                                                                                                                                                                                                25
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ON
REGISTRATION NUMBER: 33,875
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324 0880
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                              MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                             540.00
100.00%
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81.82%
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Query Match:
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                                                                                                     ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys
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                                                                                  ACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCCGGTCGCTCGATTGGACCAAG
                                                                                                                                                 GTCACACTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTC
                                                                                                                                                                                                                   CTGCCGCTCCGCGGTAAGCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCT
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                                  ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC_Compatible
COMPUTER: IBM PC_FOSN/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Defilinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Pablan, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus
5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r62kDa, 56.5
                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 525 amino acids
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERISTICS
 NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:
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100.00%
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79.55%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rercent Similarity:
Best Local Similarity: 1
Ouery Match:
                                                                                     STATE: CA
                                                                                                       COUNTRY:
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GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGGATAGCCCTCACC
                                                                       GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG
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MCAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/09769066 Patent No. US20020107360A1 GENERAL INFORMATION;
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US-09-769-066-27
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                 481 ProvalSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuJeuGlu
                                                                                     501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg
                                                                   GATACCTTGGACTACCCTGCCGGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC
                                                                                                                                                                                                                                                                                  APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr.-Shin
Purdy, Michael A.
Tam, Albert W.
TILLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKNOWN>
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                  Sequence 17, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 436 amino acids TYPE: amino acid
                                                                                                                                   CCCCTTGGCCTTCAG 1908
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   521 ProLeuGlyLeuGln 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
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STATE: CA
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                                                                                                    HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluAla
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Alignme Pred. N Score: Percent Best Lo Query M	nment Scores: 0	301 1633 321 1693
-60-	851-410A-6_COPY_5147_7129 (1-1983) x US-10-165-868-17 (1-436) 673 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCGGCATAGCCTCTGAGCTT 7	
원 상 원	1 ASNSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 20 733 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGGGGCTCCGTCGAGACCTCT 792 [	1813 TCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGGCCCATACTTTTGAT 
S d	793 GGGGTGGCTGGGGGGGCTACCTCTGGTTATGCTTTGCATACATGGCTCACTC 852 	1873 CATTICTGCCCAAAGTGCCGCCCCTTGGCCTTCAGGGCTGCCCTTTCCAGGCTGCCCTTTCCAGGCTGCCCTTTCCAGGCTGCCCTTTCCAGGCTGCCTTTCCAGGCTGCCTTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy Op	953 GTAAATTCCTATACTAATACACCCTATACCGGGGCCCCTCGGGCTGTTGGACTTTGCCCTT 912 	Oy 1933 GCTGAGCCTCTAAAATGAAGATGAGCTGAGAGTTG 1980  Db 421 AlaGluLeuGlnArgLeuLysWalGlyLysThrArgGluLeu 436
\$ q	913 GAGCTTGAGTTTGGCAACCTTACCCCGGTAACACCAATACGCGGGGTCTCCCGTTATTCC 972 	ABS-10-381-770-1     Sequence   Application US/10381770   Publication No. US20040052813A1
ζζ QΩ	973 AGCACTGCTCGCCACCGCTTCGTCGCGGTGCCGGACGGGACTGCCGAGCTCACCACCACG 1032 	; GENERAL INCORMATION:  A APPLICANT: YANG SHENG TANG COMPANY, Ltd.  ; TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS;  ; TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
oy GD	1033 GCTGCTACCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 1092 	KENCE: IECOLOU3/PCT PPLICATION NUMBER: ILING DATE: 2003-0 SEQ ID NOS: 12
Qy Dp	1093 GGCCGCGGGGATAGCCCTCACCCTGCTTGAACACTCTGCTTGGCGGCCTGCCG 1152 	SOFTWAKE: Patentin Version 3.1 ; SEQ 110 1 ; LENGTH: 660 ; TYPE: PRT
ر م	1153 ACAGAATTGATTCGTCGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 1212 	Sories Sories Sories Sories Scores:
o o	1213 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 1272 	d08.00 larity: 99.80% imilarity: 99.80%
yo, da	1273 ATTGCAATCCCGCATGACATTGACCTCGGGGAATCTCGTGTGGTTATTCAGGATTATGAT 1332 	UNETY MALCH: 01.824 INVERE: 0 DB: US-09-851-410A-6_COPY_S147_7129 (1-1983) x US-10-381-770-1 (1-660)
\( \frac{1}{2} \)	1333 AACCAACATGAACAAGATGGGCGACGGCTTCTCCCAGCCCCATGGGGCCCTTTCTCTGTC 1392 	Oy 289 GCCTCACGTCGTAGCTACCACAGCTGGGGCCGCGCGCTAACCGCGGTCGCTCCGGCC 348
ζζ qα	1393 CTTCGAGCTAATGATGTGCTTTGGCTCTCACCGCTGCCGAGTATGACCAGTCCACT 1452 	Qy         349 CATGACACCCGCCAGTGCCTGATGTCGACTCCCGGGGCATCTTGCGCCGGCAGTAT 408           Db         117 HisaspthrProProValProAspValAspSerArgGlyAlaileLeuargArgGlnTyr 136
yo, du	1453 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 1512 	Qy         409         AACCTATCAACATCTCCCCTTACCTCTTCCGGGCACCGGCACTAACCTGGTTCTTTAT 468
\$ Q	1513 ACCGGCGCGCGCGTTGCCCGGTCGATTGGACCAAGGTCACACTTGACGGTCGC 1572 	Oy 469 GCCGCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGCCACCATATAATGGCC 528
Š	1573 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 1632	Oy 529 ACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCG 588

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TACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGG 1728
                                                                               CACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGTGCTGGTCCCGTCTCCATTTCT 1788
                                                                                             537 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly
                                          MCAtee, C. Patrick
Yarbough, Patrice O. Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-09-769-066-17 (1-327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fabian, Gary R. REGISTRATION UNDRER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/542,634
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                              Sequence 17, Application US/09769066 Patent No. US20020107360A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 327 amino acids TYPE: amino acid
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STATE: CA
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Best Local Similarity:
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                                                                                            ACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTC
                                                                                                                   ThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIleLeuVal
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Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TILE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                           ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr-Shin
                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                        STATE: CA
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DB:
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              GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 1059
                                                                      TATITIACTACTACTAATGGTGTCGCTGAGATCGGCCGCGGGATAGCCCTCTCTTC 1119
                                                                                                                            1120 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 1179
                                                                                                                                                                                     1180 CAGCIGITCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 1239
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                             1 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLySAspLeu
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US-10-165-868-15
; Sequence 15, Application US/10165868
; Publication No. US20030143241A1
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COMPUTER: FLORDY disk
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUME-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUME-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUME-1989
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-165-868-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity:
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Sequence 12, Application US/10381770

Publication No. US20040052813A1

GRNERAL INFORMATION:
APPLICANT: YANG SHENG TANG company, Ltd.
TITLE OF INVENTION: THE POLYBEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPO
TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REPERENCE: IEC010037PCT
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Mismatches:
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CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                               TYPE: PRT
, ORGANISM: hepatitis
US-10-381-770-2
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Best Local Similarity:
Query Match:
DB:
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Publication No. US20040052813A1

GENERAL INFORMATION:

APPLICANT: YANG SHENG TANG company, Ltd.

TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS

TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS

FILE REPERENCE: IEC010037PCT
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APPLICAVT: YANG SHENG TANG COMPANY, Ltd.

TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOSITITE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REFERENCE: IECO10037PCT
CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Mismatches:
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Matches:
   CURRENT APPLICATION NUMBER: US/10/381,770 CURRENT FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 SEQ ID NO 4
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; Publication No. US20040052813A1
; GENERAL INFORMATION:
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                                                                                                      ORGANISM: hepatitis
                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                            LENGTH: 389
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Publication No. US20040052813A1
GENERAL INFORMATION:
TIPLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REFERENCE: IEC010037PCT
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CURRENT APPLICATION NUMBER: US/10/381,770 CURRENT FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 12 LENGTH: 232 LENGTH: 232
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; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: hepatitis E virus
US-10-381-770-3
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Search completed: August 16, 2004, 14:29:20 Job time: 122.324 secs

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Sequence 14, Appl
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Sequence 52, Appl
Sequence 92, Appl
Sequence 167, App
Sequence 167, Appl
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Sequence 25, Appl
Sequence 26, Appl
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Sequence 17, Appl
Sequence 15, Appl
Sequence 199, Appl
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Sequence 16, App
Sequence 176, Ap
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Sequence 12, Appl.
Sequence 2, Appl
                                                                                                                                                                                                                                                                                                                                                           Sequence 199,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 176,
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Sequence 175
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                                 Sequence 1,
                                             Sequence 1,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                             US-09-769-066-25
US-09-769-066-25
US-09-769-066-27
US-09-769-066-26
US-09-769-066-26
US-09-769-066-26
US-09-769-066-28
US-09-769-066-28
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US-10-165-888-18
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US-09-468-147-206
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US-10-319-745-207
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US-10-168-868-20

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US-09-468-147-167

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US-10-165-868-15
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US-09-468-147-200
US-10-319-745-199
US-10-319-745-200
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US-11-165-868-16

US-09-468-147-176

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STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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Patent No. US20020107360A1
GENERAL INFORMATION:
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  ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compugen Ltd.
                                                      - protein search, using frame_plus_n2p model
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Query Match Length DB

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                          Virus (Burma
                                                                                  NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFRAX: (415) 324-0960
 APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
                                   PRIOR APPLICATION DATA:
RAPLICATION NUMBER: 08/542,634
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
OKIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1
                                                                                                                                                                                 LENGTH: 660 amino acids TYPE: amino acid
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Matches:
Conservative:
Mismatches:
Indels:
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&
                                                                                                       ID NO:
                              LENGTH: 660 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-09-851-410-8
 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
No. US20030124510A1-A/No. US20030124510A1-B Hepatitis Viral
NUMBER OF SEQUENCES: 20
                                   1740
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                                                                                                                                                                                                                                         CATACTITIGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCCTTCAGGGCTGCGCTTTC 1920
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                                  1681 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
                                                       TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla
                                                                                                      ATTICCACTIACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTICTGCGGTTGCCGTT
                                                                                                                        581 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 4600-0183.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,410
FILING DATE: 07-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/128,275
FILING DATE: cURKNOWN
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/316,672
FILING DATE: 11-APR-1989
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Yarbough, Parrice O
Bradley, Daniel W
Krawczynski, Krzysztof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09851410 Publication No. US20030124510A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tam, Albert
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STATE: CA
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CAGTCTACTGTCGCTGAGCTTCAGCGCCCTTAAGATGAAGGTGGGGTAAAACTCGGGGAGTTG 1980
                                  641 GlnSerThrValAlaGluLeuGlnArgLeuLySMetLysValGlyLysThrArgGluLeu 660
                                                                                                                                                                                                               Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TILE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SECUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEACHTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
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19:
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Matches:
Conservative:
Mismatches:
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NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAN: (415) 324-0960
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 505, 888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420, 921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367, 486
FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336, 672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208, 997
FILING DATE: 17-JUNE-1989
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                                                                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                               US-10-165-868-19
; Sequence 19, Application US/10165868
; Publication No. US20030143241A1
; GENERAL INFORMATION:
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Bradley, Daniel
Twu, Jr-Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 660 amino ac TYPE: amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity:
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Pred. No.:
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                                 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACGGGTGCCCTCGGGCTGTTG
                                                    AspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgVal
                                                                                                                                                                                                                                                                                                    GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
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261 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle
                                                                                                   GACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACACAATACGCGGGTC
                                                                                                                                                                                                                                    CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
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AspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgVal
                                                                                                      CTCACCACCACGGCTGCTACCCCGCTTTATGAAGGACCTCTATTATTACTAGTACTAATGGT
                                                                                                                                                                       ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr
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Conservative:
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Indels:
Gaps:
 CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 660
TYPE: PRT
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                                                                                                 Sequence 1. Application US/10257044

Sequence 1. Application US/10257044

Publication No. US20030220475A1

GEMERAL INFORMATION:

APPLICANT: The Government of the United States of America, as

APPLICANT: Human Services, Centers for Disease Control and Prevention

APPLICANT: Human Services, Centers for Disease Control and Prevention

APPLICANT: HUMAN NA FIELDS

APPLICANT: YURI E. KHUDYAKOV

APPLICANT: YURI E. KHUDYAKOV

APPLICANT: JIHONG MENG

CURRENT BILLING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: 60/1957,044

PRIOR APPLICATION NUMBER: 60/1957,044

PRIOR PAPLICATION NUMBER: 60/195,380

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Vergion 4.0

SEQ ID NO 1

LENGTH: 660
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                                                                                                                           660
617
22
0
                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                          Gaps:
                                                                                                                           3.81e-229
3221.00
96.67%
93.48%
88.27%
TOPOLOGY: linear
                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                             Scores:
                                                                              US-09-769-066-14
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                               CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG 1620
                                                                                              CTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT 1680
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                                                                                                                 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn
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                                                                                                                                                            TATAACACCACTAGCGACCAACTGCTTGTCGAGAATGCCGCCCGGGCACCGGGTCGCT
                                                                                                                                                                                                                         ATTICCACITACACCACTAGCCTGGGTGCTCCCGTCTCCATTICTGCGGTTGCCGTT
                                                                                                                                                                                                                                        Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 660 amino acids
    TYPE: amino acid
    STRANDEDNESS: Hepatitis E Virus (Mexico Strain) ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769.066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/542,634
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McAtee, C. Patrick
Yarbough, Patrice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-769-066-14
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Krawczynski, Krzysztof Z.
DF INVENTION: Hepatitis E Virus Vaccine and Method
OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/870,985A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKnown>
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBRE-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 1-UUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                   Sequence 20, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION:
                                                                                                                                                    Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
                                                                                                                                    APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 659 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20:
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96.21%
93.03%
87.54%
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                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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STATE: CA
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Best Local Similarity:
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                                                                                                                                    TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020
                                                                                                                                                                                                                                                                                                                                            GGCGGCCTGCCGACAGAATTGATTTCGTCGCTGGTGGCCAGCTGTTCTACTCCCGTCCC 1200
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                                                                                      GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
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Publication No. US20040101820A1
Publication No. US20040101820A1
Publication No. US20040101820A1
APPLICANT: KABUSHIKI KAISHA TOSHIBA
TITLE OF INVENTION: Polynucleotide probe and primer derived from
TITLE OF INVENTION: from Japanese, chip including the same, kit
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REPERBUCE: 02S074A1P
CURRENT APPLICATION NUMBER: US/10/239,090A

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CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                         E Virus JAK-Sai (ORF2)
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: JP2001-191837
; PRIOR FILING DATE: 2001-06-25
; WUMBER OF SEQ ID NOS: 57
; SEQ ID NO 57
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Hepatitis E Virus JAK-Sai (ORF2 US-10-239-090A-57
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95.90%
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       TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA
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                                                                                              APPLICANT: AABCHINK RAISHA TOSHIBA
APPLICANT: RABCHINK RAISHA TOSHIBA
TITLE OF INVENTION: Polynuclectide probe and primer derived from J
TITLE OF INVENTION: from Japanese, chip including the same, kit:
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REFERENCE: 0280741P
CURRENT APPLICATION NUMBER: US/10/239,090A
CURRENT FILING DATE: 2003-07-24
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 510
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Conservative:
Mismatches:
Indels:
Gaps:
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US-10-239-090A-51
Sequence 51, Application US/10239090A
Publication No. US20040101820A1
GENERAL INFORMATION:
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ORGANISM: Hepatitis
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US-10-239-090A-55

US-10-239-090A-55

Sequence 55, Application US/10239090A

Publication No. US20040101820A1

GENERAL INFORMATION:

APPLICANT: KABUSHIX KAISHA TOSHIBA

TITLE OF INVENTION: Polynucleotide probe and primer derived from hepatitis E virus oc

TITLE OF INVENTION: detecting hepatitis B virus using the same,

TITLE OF INVENTION: detecting hepatitis B virus using the same

TITLE OF INVENTION: detecting hepatitis B virus using the same

TITLE OF INVENTION NUMBER: US/10/239,090A

CURRENT APPLICATION NUMBER: US/10/239,090A

CURRENT FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 57

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US-10-239-090A-55
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Best Local Similarity:
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Pred. No.:
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TYPE: PRT
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APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
TAPLICANT: Dawson, George J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE REPREBENCE: 6222.018. P.
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
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Alignment Scores:  Pred. No.: Score: Score: Score: Bercent Similarity: 95.45\$ Conservative: 26 Best Local Similarity: 91.50\$ Mismatches: 30 Query Match: 10 Gaps: 0	-09-851-410A-6_COPY_5147_7129 (1-1983) x US-09-468-147-167 (1-660)  1 ATGCGCCTTCGGCTATTTTGTTGCTCCTCATGTTTTTGCCTATGCTGCCCGCGCCA	Db 1 MetArgProArgAlaValLeuLeuLeuLeuLeuLeuLeuLeuProMetLeuProAlaPro 20 Oy 61 CCGCCGGTCAGCCGTCTGGCCGTCGTGGGCGCGCAGCGGGGTTCCGGCGGTGGT 120 Db 21 ProAlaGYCInProSerGYVATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	181 CCCTTCGCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTGTGTTCGCCAACCCGCC	241 CGACCACTCGCTTGGCGTGACCAGGCCCAGGCCCGCGTTGCCTCACGTCGT	ACCCCG 3	4 -	421 TCTCCCCTTACCTTGCCTGCCCACCGCACTAACCTGCTTTTATGCCGCCCCTCTT 48  [421 TCTCCCCTTACCTTGCGTGGCCACCGCACTAACCTGCTTCTTTATGCCGCCCCTCTT 78  [431 SerProlenthySerSerValalaSerGlyThragienivallentvralaalaprolenth	481 AGTCCGCTTTTACCCCTTCAGGACGACCAATACCCATALAATGCCCACGGAGCTTCT 54  161 AGTCCGCTTTTACCCCTTCAGGACGACCAATACCCATALAATGCCCACGGAGCTTCT 54  161 AGTCCGCTTTTACCCCTTCAGGACGACCAATACCCATALAATGTATTACTTCT 54	541 AATTATGCCCAGTACCAGTTGCCCGTGCCACAATCCGTTACCGCCGCTGGTCCCCAAT 60	GCTGTCGGCGGTTACGCCATCTCCATCTTCTGGCCACACACA	661 TCGTTGATATGAATAACTTGACATGTTGTATTTTAGTCCAGCCGGCATA 72 [	721 GCCTCTGACTTGTATCCCAAGTGACGCCTACCTACGTACCTACGTGCTCC 78  AAASSEGULAUVAIIEPENSSEGULASTVAACASGGGGGTCC 78  241 AAASSEGULAUVAIIEPENSSEGULASTVAACASGGGGGGTCC 78	GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTTATGCTTTGCATA 84		901 GACTTTGCCTTGAGCTTTGCGAACCTTACCCCGGTAACACCAATACGGGGTC 96

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                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa = Unknown or Other at position 84
OTHER INFORMATION: Xaa = Unknown or Other at position 230
CHER INFORMATION: Xaa = Unknown or Other at position 447
US-10-319-745-167
                                                                                                             DETECTING
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Erker, James C.
APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
CURRENT APPLICATION NUMBER: US/09/468,147A
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: US PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 167
TABLETTER FOR THE FARE OF SEC ID NOS: 258
TABLETTER OF SEC ID NOS: 258
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Matches:
Conservative:
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ORGANISM: Hepatitis E Virus
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Query Match:
DB:
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Search completed: August 16, 2004, 13:33:17 Job time: 137.324 secs

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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOOJ381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: US/10/170,205E
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 35792
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16484, A
34948, A
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37443, A
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7552, Ap
17307, A
1618, Ap
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22224, A
421, App
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4, Appli
3, Appli
3, 2969, B
33190, B
33191, A
33191, A
92, Appl
93, Appl
94, Appl
7582, Ap
19874, A
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US-10-425-115-313976
US-10-425-115-313976
US-10-170-205E-16484
US-10-170-205E-34948
US-10-170-205E-34948
US-10-170-205E-34941
US-10-425-115-313979
US-10-425-115-313979
US-10-425-115-313979
US-10-704-781-4
US-10-704-781-4
US-10-704-781-3
US-10-170-205E-33199
US-10-170-205E-33199
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PCT-USO4-10531-93
PCT-USO4-10531-93
PCT-USO4-10531-93
US-60-581-351-7582
US-10-170-205E-18774
US-10-170-205E-37579
US-10-170-205E-37579
US-10-170-205E-31645
US-60-568-073-902
US-10-170-205E-37443
US-10-170-205E-37443
US-10-170-205E-39078
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US-60-581-351-7552
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US-60-581-351-7553
US-10-170-205E-22224
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Best Local Similarity:
    RESULT 1
US-10-170-205E-35792
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US-10-170-205E-35792
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-MODEL=frame+ n2p.model - DEV=xlp
-MODEL=frame+ n2p.model - DEV=xlp
-Q=/cgn2 1/USFTO_spool p/US09851410/runat 16082004_125455_8586/app_query.fasta_1.4238
-Q=/cgn2 1/USFTO_spool p/US09851410/runat 16082004_125455_8586/app_query.fasta_1.4238
-DB=Pending Patents AA New -QFWT=fastan - SUFFIX=n2p.rapn - MINMATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITS=bits -STRAT=1 - END=-1 - MATRIX=blosum62
-TRANS=buman40 - Cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100
-TRR MIN=0 - ALIGN=15 - MODE=LOCAL -OUTFMT=pct - NORM=ext - HBAPSTZR=500 - MINLEN=0
-MAXLEN=200000000 - USER=US09851410 @CGN 1 1 95 @runat 1608204 125455 8586
-LOOPCR=0 - ICPU=3 - NO MMAP - LARGEQUERY NEG SCORES=0 - MATR - DSPBLÖCK=100
-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 7551, Ap
Sequence 7551, Ap
Sequence 19858, A
Sequence 1197, Ap
Sequence 185, App
Sequence 280165,
Sequence 249, App
Sequence 249, App
Sequence 249, App
Sequence 249, App
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(without alignments)
11860.500 Million cell updates/sec
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11. /cgn2 6/ptodata/2/paa/PCT_NEW_COMB.pep:*

22. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

33. /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

44. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

55. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

67. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-170-205E-19858
US-60-581-351-7586
US-60-581-351-7586
US-60-591-969-185
US-10-425-115-280165
PCT-USOZ-22858A-249
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CAGCAGIACTCGAAGACCITCTTTGICCTGCCGCTCCGCGCGTAAGCTCT-----CT 1638
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                                                                                                                                                                                      1048 ATGAAGGACCTCTATTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCC 1107
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| AspGlyLeuValIlePro-----ValThrAlaAlaGluCysProAlaIleProValThr 595
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                                                                                                                                                                                                                                                           541 ValValSerValThrProAlaAspGlyArgVal11e------ProValAlaSerAla
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694 lThrSerAlaAspGlyProValPheSerValThrSerAlaAspSerSerValValProVa
                                          AACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTTATTCCAGCACTGCTCGCCAC
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                      --CCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGC
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                                                                                            -----ThrProAlaAspSerPro----
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163
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Conservative:
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|AsnGlyIleLeuVal-----
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                         ; ORGANISM: Homo sapiens
US-10-170-205E-18914
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372) B
FULS REFERENCE: 38-21(53372) B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
LENGTH: 763
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LeuAlaProProLeuProProAlaProProGluAlaProArgGluSerArgProAlaLeu 95
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Conservative:
Mismatches:
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                                                                                          5-60-581-351-7551
Sequence 7551, Application US/60581351
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Myco
US-60-581-351-7551
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Pred. No.:
1840
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216 aProProProProAlaileSerLeuAenAlaProSerTyrAsnTrpGlyAlaAlaie 236 205 GCGGCCGGGGCGCGGACCTGGTCTCGCCACCCGCCCGCCCCCCCCCC	### OTTO TO THE CONTROLL OF TH
PROTEIN PROTEI	
TACTCCAAGACCTTCTTTGTCCTGCCGCTCCGCGTAAGCTCTTTCTGGGA 1646  OTEDThrThrProProLeuAla	Best Local Similarity: 23.78%   Mismatches: 342

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466 TATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCCATATAATG 525
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                                                                                                                                                                                             APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In )
FILE REPRENCE: 38-21 (53372) B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US/60/479,962
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SEQ ID NO 7586
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                        1882 CCAGAGTGCC---GCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTA 1927
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; Sequence 7586, Application US/60581351
; GENERAL INFORMATION:
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                                          CGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTTATTCCCAGCACTGCTCGC
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| 651 oSerGlyGluProPheSerGlyLeuGlyAspLeuSerProLeuLeuPheProProLeuSe
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			RESULT 6 US-60-568-073-1197 ; Sequence 1197, Application US/60568073 ; GENERAL INPORMATION: ; APPLICANT: Huang, Fei ; APPLICANT: Shaw, Peter ; APPLICANT: Clark, Edwin	; TITLE OF INVENTION: COLON CANCER BIOMARKERS ; FILE REFERENCE: 10205 PSP: ; CURRENT APPLICATION NUMBER: US/60/568,073 ; CURRENT FILING DATE: 2004-05-04 ; NUMBER OF SEQ ID NOS: 1305 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 1197 ; LENGTH: 5179 ; TYPE: PRT ; ORGANISM: Homo sapiens US-60-568-073-1197	Alignment Scores: 0.000109 Length: 5179  Pred. No.: 0.000109 Length: 5179  Score: 192.00 Matches: 149  Percent Similarity: 22.51\$ Mismatches: 261  Query Match: 5.26\$ Tidels: 178  DB: 7 Gaps: 33	CTTCGCAACCCTATATTCAACCAACCAACCCCT
Oy 526 GCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGC 585	Qy         706 GTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAAC 765           Db	826 GTTATGCTTTGCATACATGGCTCACTGTAAATTCCTAT 86  1	OD 259 U	1078 GGTGTCGGTGAGATCGGCCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTG	Db 327 ProAlaSerLysProSerProProThrProProAlaProProGlubroAsnAsnVal 345  Qy 1258 CAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGT 1311  Db 346 ProProSerProProIleProProAlaProProProProSerGlyLeu 361  Qy 1312 GTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCC 1371  Db 362	Oy 1372 CCATGGGCCCTTTCTCTGTCTTC

Db 1790 yTrpLeuAspSerGlyLysProAsnPheHisLysPro-GlyGlyAspT 1806  Qy 1154 CAGAATTGATTTCGTCGGCTGGCCAGCTGTTCTACTCCCGTTCGTT	Qy 1214 ATGGCGAGCCGACTGTTAAGTTGTATACATCTGTA	Qy 1249	Qy 1277 CAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTTA 1318	1319 TTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG	OY 1360CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGC 1411  Db 1890 hrGluAenProThrProProThrThrThrThrProlleThrThrThr 1904	Qy 1412 TTTGGCTCTCTCACCGCTGCCGAGTATGACCAGTTCACTTGTGGCTCTTCGACTGGCC 1471	Qy 1472 CAGTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCG	Qy 1532 CCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCTCTCCACCATCCAGC 1591 :::	Oy 1592 AGTACTCGAAGACCTTCTTGTCGGCGCTCCGCGGGTAAGCTCTCTT 1639	Oy 1640TCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATATAACACCACTG 1693	Qy 1694 CTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTGCTATTTCCACTT 1750	Qy 1751 ACACCACTAGCCTGGGTGCTGGTCTCCGTTTCTGCGGTTGCCGTTTTAG 1804	Oy 1805 CCCCCACTCTGGGCTAGCATTGCTTGAGATACCTTGGACTACCCTGCCGGGCCCATA 1864	Qy 1865 CTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTCCA 1922 :::                :::       Db 2040 ThrThrThrThrThrValThr-ProThrProThrProThrGlyThrGlnThrPro 2057	ESULT 8 \$-10-425-115-280165 Sequence 280165, Application GENERAL INFORMATION:	; APPLICANT: La Kosa, Thomas J. ; APPLICANT: Zhou, Yihua ; APPLICANT: Zhou, Yihua ; APPLICANT: Cov, Yongwei ; APPLICANT: Cov Xongwei ; APPLICANT: Cov Xongwei	TILE OF INVENTION: Plants TILE OF INVENTION: Plants FILE REFERENCE: 38-21 (53222)B
-09-851-410A-6_COPY_5147_7129 (1-1983) x US-60-591-969-185 (1-5179) 143 CTCAGCCCTTCGCAATCCCTATATTCATCCAACCAACCCCTTCGCCCCCG 19	1508 IleThrProProAlaSerThrThrThrLeuProProThrThrThrProSerProFroThr 15 194ATGTCACCGCTGCGGGCTGGACCTCGTG 22 :::	Db 1528 ThrThrThrThrThrProProProThrThrThrProSerProProThrThrPro11e 1547  Qy 227 TICGCCAACCGCCGACCACCGCTGGCTGGGCGTGACCAGGCCCAGGCCCCG 283  hb 1548	284 CCGTTGCCTCACGTCGTAGACCTACACACACGCGCGCGCG	344 CGGCCCATGACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATCTTGC 39	398	458 IGGTICTTTAIGCGCCCCTCTIAGICCGCTTTTACCCCTICAGGACGCACAATACCC	518 ATATAATGGCCACGGAAGCTTCTAATTATGCCCAGATACCGGGTTGCCCGTGCCACAATCC	578 GTTACGGCCGGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCAGC 63	DD 1662 INFINITIONEPROSERPTOPIOLIEINFINITIONEPROPEOPROFINITIONEPRO 1681  QY 638 CACAGACCACCACCACCACCGACGTTGATATGAATACAATAA 682  Dh 1682 carcarbrollamhrmhrmhrmhrmhrmhrmhrmhrmhrmhrmhrmhrmhrm	683 CCTCGACGGATGTTCGATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAA  1.::   ::::   :::	743 GIGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCGGGGGCTGGCT	803 AGGAGGAGCTACTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCT	863 ATACTAATACCCTATACCGGGCCTGTTGGACTTTGCCCTTGAGTTGAGT	1/33	Qy 974 GCACTGCTCGCCACCGCCTTCGTCGCGGACGGGACTGCCGAGCTCACCACCACGG 1033	Qy 1034 CIGCTACCGCTTTATGAAGGACCTCTATTTACTAGTACTAATGGTGTCGGTGAGATCG 1093  Db 1782	Qy 1094 GCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTGGCGGCCTGCCGA 1153

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974 GCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACCGGGACTGCCGAGCTCACCACCACGG 1033
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232 LeubroSerProProValGlnGlnProProArgThrProlleLeuProProSerArgLys 251
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     803 AGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCT
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: PCT/US02/22858A CURRENT FILING DATE: 2002-07-19
PRIOR PAPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-03-07
PRIOR PAPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-18
PRIOR FILING DATE: 2000-05-18
PRIOR PRING APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
                             ; Sequence 249, Application PC/TUS0222858A; GENERAL INFORMATION:
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SEQ ID NO 249
LENGTH: 1250
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Yang, Yonghong
Weng, Gezhi
Zhang, Jie
Ren, Felyan
Xue, Aidong J.
Wang, Jian-Rui
Wehrman, Tom
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                           Sequence 18875, Application US/10170205E
GENERAL INFORMATION:
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TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CLOR1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PATECRIFIN version 3.2
SOFTWARE: PATECRIFIN version 3.2
SEQ ID NO 18875
LENGTH: 5262
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Best Local Similarity:
Query Match:
DB:
             US-10-170-205E-18875
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Page 13

	CTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCG	CAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCA	12/4 TIGGRAFIC CUCGCATCACT TO ACCITUGATO A TIGGRAFIC TO A TIGGRAFI	1370 CCCCATCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCACCG   1429   834
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Db 902 GlyGlnGlySerFroCysGluGluGluBroArgAlaProvalAla 918  Qy 1772 GTCCGTCTCTTCTGCGGTTGCCGTTTTAGCCCCCACTCTG 1816     :::	Alignment Scores:  Pred. No.:  182.00  Matches: Score:  138  Score:  13.12\$  Conservative: 54  Best Local Similarity: 22.37\$  Mismatches: 176  Query Match:  6 99\$  US-09-851-410A-6 COPY 5147 7129 (1-1983) x US-10-896-891-303 (1-5262)	149 CCTTCGCAATCCCTATATTCATCCAACCAACCCTTCGCCCCCGAT          :::     :::	Oy 266 ACCAGGCCGGCGGCGGTGGCTCGTAGACCTACCACAGGGGGGGG	CCGGCACTAACCTGGTTCTTTATGCCGCCCTCTTAGTCCGCTTTTACCCCTTCAGG

Qy 308 CCACAGCTGGGCCGCCGCTAACCGCGGTCGTCCGGCCCATGACCCCGCCAGTGC 367  Db 485 ProLyshladlyThrAspAlaAlaProProProAlaValProLysAlaProSerAspG1y 504  Qy 368 CTGATGTCGACGCGCGCATCTTGGCCGGCAGTATAACCTATCAACATCTCCCC 427  :::	540ArgalaalaProProSerAsnGlualaThrProAlaval 515 CCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTG	Qy         617 CCATCTCCA	630 SerSerProValAlaSerAlaMetHisAlaLysValThrProArgProLeuProAlaSer 716GGATAGCCTCTGAGCTTGTGATCCCAAGTGAGGCCTACACTATC 716	Db 670 AlaThrAsnAlaAlaSerProGlyAlaLysProGluAlaAlaGlyG 685  Qy 821 GTCTTGTTATGCTTTGCATACATGGCTCACTGGTAAATTCCTATACTA 868	929 ACCTTACCCCGGGTACACCAATACGGGGGTCTCCCGTTATTCCAGCACTGCTCGCCACC	723ProMetGlyAlaGlyAlaThrGlnMetSerProThrGlyAla 1049 TGAAGGACCTCTATTTACTAGTAGTAGTGTGTGTGTGAGATCGGCGGGGGATAGCCC 138AlaAsnThrHisMetSerProIleGlyAlaGlyAlaT	Qy 1109 TCACCCTGTTCAACCTTGCTGACACTTGCTTGGGGGCCTGCCGA 1153 :::
Db   868	RESULT 12 US-10-851-438-79  Sequence 79, Application US/10851438  GENERAL INFORMATION: APPLICANT: Curaden Corporation APPLICANT: Vernet, Corine A.M. APPLICANT: Pernandes, Elma R. APPLICANT: Taupier, Raymond J. APPLICANT: Taupier, Raymond J. APPLICANT: Ginn, Kerry B. APPLICANT: Spytek, Kimberly A.	# APPLICANT: Rastelli, Luca # APPLICANT: Herrman, John L. # TITLE OF INVENTION: Novel Proteins and Mucleic Acids Encoding Same # TILE REFERENCE: 15966-750 # CURRENT APPLICATION NUMBER: US/10/851,438 # CURRENT PILING DATE: 2004-05-21 # PRIOR PILING DATE: 2001-04-30 # PRIOR FILING DATE: 2001-04-30 # PRIOR FILING DATE: 2001-04-03 # PRIOR FILING DATE: 2001-04-03	APPLICATION FILING DATE: R OF SEQ ID NG ARE: Patentin NO 79 TH: 1151 : PRT NISM: Gallus G	Alignment Scores: 0.000428 Length: 1151 Score: 180.50 Matches: 163 Score: 31.23 Conservative: 65 Best Local Similarity: 22.33 Mismatches: 258 Query Match: 6 Gaps: 33	US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-10-851-438-79 (1-1151)  QY 80 GCCGCGTCGTGGGCGCCAGCGGCGTTCCGGCGTTCTGGGGTGCTG 139  Db 392 AlaAlaThrValProThrAlaGlyAlaValProLysAlaSerThrGlyThrThr 409	OY 140 ATTCTCAGCCTTCGCAATCCCTATATTCAACCAACCAACC	191CCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCCCG

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Matches:
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US-10-425-115-313976
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NAME/KEY: unsure
LOCATION: (1) . (708)
OTHER INFORMATION: un
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exeraic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yordan
APPLICANT: Shou, Yordan
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 [3322] B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 313976
LENGTH: 708
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Sequence 260103, Application US/10425115
Sequence 260103, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICANTON UNBER: US/10/425,115
CURRENT PRING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Mismatches:
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OTHER INFORMATION: unsure at all Kaa locations
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Matches:
              1870 GATGATTTCTGCCCAGAGTGCCGCCCCC 1897
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                                                ----ValSerSerProProAlaThrPro 479
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Best Local Similarity:
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ORGANISM: Zea mays
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                                                                                                      US-10-425-115-260103
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 260103
LENGTH: 317
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                                                                                                                                                                              CCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCG--- 1018
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                                                                                                                             SerLysProFroSerSerProGluLysProSerProProLysGluProValSerSerPro 247
                                 ---CACCCTATACCGGTGCCCTCGGGCTGTTGG 901
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                                                                     208 ProProThrLeulleProSerProProProGlnGluLysProThrProProSerThrPro
                                                                                                        902 ACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGGTAACACCAATACGCGGGTCT
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AlaAlaProSerMetSerValArgGlyGlyGlyAlaGlyGlnPro 786	GCTGAGGAGGAGGAGCTCTCGTTATTATGCTTTGCATACATGGCTCACTCGTAAAT 858		TCCT	AlaGlnProProSerLysIleIleGlnLeuThrProValProVa 816	GCCCTCGGGCTGTTGGACTTTGCCCTTGAGTTTCGCAACCTTACCCC 939	GGTAACACC	roGlnLysValLeuLeuProSerSerThrArglleThrTyrVal 852	TCCAGCACTGCTCGCCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020	:::  ThrValThrSerTyrGlyProThrSerSerValAlaLeuGlyPheThrSer 889	GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCTGTTCAAC	:::    LeuGlyProSerGlyProAlaPheValGlnProLeuLeuSerAlaGlyGlnAlaProLeu 909	GAATTGATT	TCGTCGGCTGGTGGCCAGCTGTTCTAC	CAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAG 1251	:::  SerAlaProLeuAlaGlnProSerGlnAlaProProSerLeuValTyrThrValAlaThr 969	AATGCTCAGCAGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGT 1311	::     aalaThr1leLeuPro	GTGGTTATTCAGGATTATGATAACCAACAAGATCGGCCGACGCCT 1362		TCTCCAGCCCCATGGGGCCCTTTCTCTTGGGGCTAATGATGAGGTTTGGCTCTCT 1422	erProPheProSerAlaThrAlaGlySerMetThrTyrSer 1008	CTCACCGCTGCCGAGTATGACCACTTATGGCTCTTCGACTGGCCCCAGTTTATGTT 1482	7 5	LysAlaAla1leAlaSerIleProvalGlySerPheGluAlaGlyAlaSer-GlyArgPr 1045	CACTTGACGGTCGCCCTCTCCACCATCCAGCAGTACTCGAAG 1602	  GlyProAlaProArgGlnProLeuGluProGlyProValArgGl 1060	GGCTCCGCGGTAAGCTCTCTTGGGAGGCAGGCACAACTAAA 1662		168	aProProProLeuProGluThrTrpThrProThrAlaArgSerSerProProLeuProPr 1096
772AlaAlaProSerMetS	799 GCTGAGGAGGAGGCTACCTCTGG			796 lProvalGlnAsnGlyAlaGlnF	886 GCCCTCGGGCTGTTGGA          816 lSerThrProSerGly	940 GGTAACACC	833 GlyProThrSerGlnProGlnLy	970 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGT	::: 873 ThrValThrSerTyrGlyProTh	1081 GTCGGTGAGATCGGCCGCGGGAT	890 LeuGlyProSerGlyProAlaPh		1165 TCGTCGGCTGGTGGCCAGCTG :::::        ::: 930 AlaAlaProGlyGlyProVall1	1192 TCCCGTCCCGTTGTCTCAGCCAA	::: 950 SerAlaProLeuAlaGlnProSe	1252 AATGCTCAGCAGGATAAGGGTAT	970 SerThrThrProProAlaAlaTh	1312 GTGGTTATTCAGGATTATGATAA	981	1363 TCTCCAGCCCCATCGCGCCCTTT :::	990 ThrProAlaProThrSerProPh	1423 CTCACCGCTGCCGAGTATGACCA		1403 ICIGACICIGITAA ::::: 1026 LysAlaAlaIleAlaSerIlePr		  1045 oGlyProAlaProArgGlnP	1603 ACCTTCTTTGTCCTGCCGCTCCG	1060 uProThrAlaE		1076 aProProProLeuProGluThr
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1135	::: 1116 rSerSerSerAspTrpArgValProGlyGlnGlyLeuGluAsnArgGlyGluProPr 1135	1116	qq
1809	1750 TACACCACTAGCCTGGGTGCTGGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCC 1809	1750	δλ
1116	1096 oProAlaGluGluArgThrSerAlaLysGlyProGluThrMetAlaSerLysPheProSe 1116	1096	qq
1749	1690 ACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGGCCGGGCACCGGGTCGCTATTTTCCACT 1749	1690	ઠે

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Aaw93388 I
Aaw93390 I
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Abj04811
Abj04807
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Aar26189
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HEV ORF2 protein
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01-MAY-1992;
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Command line parameters:
-MODEL=frame+ n.p. model - DEV=xlp
-MODEL=frame+ n.p. model - DEV=xlp
-O=/cgn2_1/USFTO_spool_p/US09851410/runat_16082004_125716_9617/app_query.fasta_1.4238
-O=/cgn2_1/USFTO_spool_p/US09851410/runat_16082004_125716_9617/app_query.fasta_1.4238
-D=A_Geneseq_29Gan04 - OFMT=fastan - SUFFIX=oli.rag - MINMATCH=0.1 - LOOPCL=0
-LIST=45 - DOCALIGN=200 - THR SCORE-quality - THR MIN=1 - ALIGN=15 - MODE=LOCAL
-OUTFWT=pto - NORM=ext - HEAFSIZE=560 - MINEND-0 - MAXIEN=200000000
-USER=US09851410_@CGN_1 1_141_@runat_16082004_125716_9617 - NCPU=6 - ICPU=3
-NO_MMAP - LARREQUERY - NEG SCORES=0 - WALT - DSPBBLOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS-1 - XGAPOP=60 - XGAPEXT=60 - FGAPOP=6
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Aar96102 E
Aar96104 E
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                 Compugen Ltd
                                           using frame_plus_n2p model
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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Length: Matches:

Conservative: Mismatches: Indels:

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Percent Similarity:
Best Local Similarity:
         Sequence 659
                           Alignment Scores:
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                                     600
                                                                   virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
                                                                                                                                    TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1977
                                                                                                                                                 SerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeu
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AsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIle
                   TCAACCTATACCACCAGGGTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTG
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00681078.
92US-0082335.
92US-00876941.
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diagnosis; HEV
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05-APR-1990;
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Query Match:
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14-FEB-1994
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The sequence is that of the putative virus capsid protein encoded by Mexico strain hepatitis B virus (HEV) open reading frame ORF2. This protein or peptide fragments of it may be used in a vaccine composition for immunising an individual against HEV. Antibodies raised against these peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen and antibody vaccines against hepatitis E virus infection - contain peptide(s) derived from capsid protein C-terminal or antibodies against protein.
                                                                                              infection; block;
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                                                                                          Hepatitis E virus, vaccine, neutralising antibodies, open reading frame; antibodies.
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                                                     Mexico strain HEV ORF2 puative virus capsid protein.
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US DEPT HEALTH & HUMAN SERVICES.
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	ArgProAlaThrAlaGlyAlaAlaAlaLeuThrAlaValAlaProAlaHisAspThrSer CCCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGFCTACT	121 ProValProAspValAspSerArgGlyAlaileLeuArgArgGinIyrAsnLeuSerinr 140 421 TCACCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTT 480	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	541 AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT 600	01 GCAGTIGGAGGCTATATCCATTTCTTTCTGGCCTCAAACACCACAACCC All	61 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA	21 Servalabhechshaeileenniseinnaspaalasjirebecvalahiitooffic 21 GCATCTGAATTGGTCATCCCAAGCGCCTTCACTACCGCAATCAAGGTTGGCGTTG 	41 Alasetolubeuvalliefloseiglumigbeurisiyrhigasholmirylipalses. 81 GTTGAGACATCTGGTGGTGGGGGGAAGCCACCTCGCGTCTTGTCATGTTATGCATA.	TACTG	01 GACTITGCCTIAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACAC 	961 TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG 1020 	1021 ACCACAACTGCAGCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080    -	1081 GGTGAAGTCGGCGGGGATAGCTCTAACTTAACCTTGCTGCTGACACGCTCCTCGGC 1140		1201 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 1260	61 GATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGTGGTCATTCAG	421 AspLysGlyValAlaIleFrOHisAspIleAspLeuGlyAspSerArgvalVaIlleGin 440 1321 GATTATGACAACCAGCATGAGCAGGATCGGCCCACCCGTCGCCCTGCGCCATCTCGGCCT 1380

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diagnosis, prevention and treatment of hepatitis E virus infection mammals, particularly humans. 

English 3A; 70pp; Example 1; Fig

This invention describes a swine hepatitis B virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine AHV can also be used for the production of strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled betweethermine. contamination

Sequence 659 AA;

ATGCGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTGTTTCTGCCTATGTTGCCCGCGCCCA ProThrGlyGlnProSerGlyArgArgArgGlyArgArgSerGlyGlyThrGlyGlyGly CCCTTTGCCCCAGACGTTGCCGCTGCGTCTGGACCTCGCCTTCGCCAACCAGCC CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGCGCCCCTCCGGCTGCCTCCGTCGC CGACCTGCCACAGCCGGGGCTGCGGCGCTGACGGCTGTGGCGCCTGCCCATGACACCTCA CCCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT TCACCCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTT AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC AATTATGCACAGTACCGGGTTGCCCGGGGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT GCAGTIGGAGGCTATGCTATATCCATTTCTTGGCCTCAAACAACCACACACCCCTACA (1-659)659 658 0 Length: Matches: Conservative: Mismatches: Indels: US-09-851-410A-10\_COPY\_5117\_7096 (1-1980) x AAW93387 Gaps: 99.85\$ 99.85\$ 84.67\$ 0 558.00 Percent Similarity: Best Local Similarity: Alignment Scores: \_ 61 21 121 181 241 81 101 361 121 141 161 41 61 301 541 181 421 481 601 Query Match: No.: ò g ઠે g δ q qq ò a ò qq ò qq g ઠે a ò g ò ò

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                                                                                                                                                                   The putative capsid protein (AAR96090) of hepatitis E virus (HEV) Mexico strain is encoded by ORF-2 (AAT27108) of the virus. PCR amplification of ORF-2 allows prodn. of capsid protein or of C-terminal regions of the capsid protein (see also AAR96092, AAR96094 and AAR96096) and expression in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector provides recombinant C-terminal regions (see also AAR96102 and AAR96104) useful as diagnostic reagents and in vaccines. The HEV Burma strain capsid protein (AAR96089) may similarly be used. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                         AsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                      ньу; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines
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Percent Similarity: Best Local Similarity:

Alignment S Pred. No.:

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62K antigen (AAR96092) comprises the C-terminal 549 amino acids of hepatitis E virus (HEV) Mexico strain capsid protein (see also AAR96090). It is obtd. by PCR amplification of HEV Mexico ORF-2 (AAR72108), insertion of amplified DMA (AAR72110) into vector polex and expression in E. coli cells. Expression of full-length ORF-2 in 5f9 insect cells using a baculovirus system also results in prodn. of 62K antigen (see also AAR96104). 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
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Hepatitis E virus (Mexico strain)
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                                                                 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT
                                                                                                                                         CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC
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Qy         1290         CGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCG         1349           Db         320         eAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspAr         340           Qy         1350         GCCCACCCCGTCGCCCTCGCGCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGAT         1409           Db         340         gProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLe         360           Qy         1410         TTGCTGTCTCCACTGCAGCAATTATACGATCCAATTATACGATCCAATTACATTGCCCC         1469		QY         1530 CCGATCGCTTGACTGGTCCAAAGTCACGTCGGCGGCCCCTCCCGACTGTTGAGCA 1589           DD         400 AATGSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGl 420           QY         1590 ATATTCCAAGACATTCTTTGTGCTCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCGG 1649           DD         420 HTYLSErLySThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGl 440	Oy 1650 CACAACAAAAGCAGGTTATCCTTATAATATATACTGACTAGTGACCAGATTCTGAT 1709	460 eGluAsnalaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGl 1770 TCCGGTCGCCATTTCTGCGCCCGCGGTTTTGGCTCCACGCCCCGGGCTCTGCTGGA 1770 TCCGGTCGCCATTTCTGCGCCGCGGGTTTTGGCTCCAGGCTCCGCCCTGGCTGG	1830 GGATACTTTTGATTATCCGGGGGGGGGCGCACATTTGATGACTTCTGCCCTGAATGCCG 188 	Qy 1890 CGCTTTAGGCCTCQAGGGTTCTGCAGTCAACTGTCGAGGCTCCAGGGCCTTAA 1949	540 8		XX XX DT 16-OCT-2003 (revised) DT 06-AUG-1996 (first entry)	DE Hepatitis E virus (Mexico strain) recombinant 62K antigen. XX X HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;	<pre>KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; KW capsid. XX XX Hepatitis E virus; Mexico strain.</pre>	PN W09612807-A2. XX XX PD 02-MAY-1996.	AA PP 23-OCT-1995; 95WO-US013703. XX PR 24-OCT-1994; 94US-00327952.
Alignment Scores:  Pred. No.:  Score:  Score:  39.00  Matches: 538  Score: 99.45\$  Conservative: 0  Best Local Similarity: 99.45\$  Mismatches: 1  Query Match: 29.48\$  Indels: 3  DB: Cop. 200 Match: 10  Cop. 200 Match: 200 Matcher Cop. 200 Matcher 200 Mat		454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGTACTAAT 41 ASTLAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGTACTAAT 41 ASTLAGTCCTGTATGATAATAATAATCCGCCTCTGCCGCTGCAGGACGTACTAAT 514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 61 ANTWELLIALIALIALIALIALIALIALIALIALIALIALIALIA	574 ATCCGTTACCGCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATACCATTTCTTTC	QY         634 TGGCCTCAAACAACCACAACCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693	754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC	814	874	Qy 934 ACCACTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTC 989 	Qy     990 CGCCCGAGGGCCCGACGGGACTGCGGACCTGCCACCACCACCACCACCACGTCATGAA 1049       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         1050         AGATCTCCACTTTACCGGCCTTAATGGGGTQAAGTCGGCCCGGGGATAGCTCTAAC         1109           Db         240         SASpLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuTh         260	Oy 1110 ATTACTTAACCTTGCTGACACGCTCCTGGCGGCTCCCGACAGAATTAATT	Oy 1170 TGGGGGCAACTGTTTATTCCGGCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAA 1229  DD 280 AGIYGINLEUPheTYrSerArgProValValSerAlaAsnGlyGluProThrValLy 300	Oy 1230 GCTCTATACATCAGAGAATCCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATAT 1289 

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DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus (HEV) Mexico strain capsid protein was cloned into baculovirus expression vector pBluBacIII and recombinant 62K was expressed in 549 insect cells. High levels of expression were obtd. and the recombinant 62K was obtd. in over 95% purity. However, C-terminal processing resulted in the deletion of 9 or 23 amino acids from 62K, giving 2 related polypeptide species (AAR96102 and AAR96101 and AAR96103). Recombinant 62K burna 62K antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                     Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
                                                                                       Zhang Y;
                                                                                    Yarbough PO,
                                                                                                                                                                                                                                     Claim 8; Page 97-98; 125pp; English.
                                          (GENE-) GENELABS TECHNOLOGIES INC.
95US-00542634.
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                                                                                                                               WPI; 1996-230608/23.
  13-OCT-1995;
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Sequence 525 AA;

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	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	0	377.00	99.438	99.43%	57.218	73
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

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•	ACG   spv	CAT 	TGC 	AGT		TGA:	TGG   euV	CTG 	CAG   rova	
tive: es: 96104	CGG LOA	CTGACATC          LeuThrSe	CTCT LOL	CAC  - - 1aG	GAG 17-C	ACA   spm	AAT  -	CAT    hrs	CTC 	
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RESULT 9

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ò	m	CCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTC 98
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λ	1170	CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAA
qa		uPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLy
δ	1230	ACATCAGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATAT
Ωp	300	rvalgluAsnAlaglnGlnAspLysGlyValAlaileProHisAspll
ΟŻ	1290	TTGGGGTGTGGCATTCAGGATTATGACAACCAGCATGAGCAGGATCG
qa		AspleuGlyAspSerArgValVallleGlnAspTyrAspAsnGlnHisGluGlnAspAr
λö	1350	GCCCACCCGTCGCCTGCGCCATCTCGCCTTTTCTGTTCTCCGAGCAAAGATGTACT 1409
QQ	340	ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLe
δλ		INGCCIGICCCTCACIGCAGCCGAGIATGACCAGICCACTIACGGGICGICAACIGGCC 1469
qq	360	TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPr
ò	1470	SCCGTAGC
qa		SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAl
ò	1530	GACTGGTCCAAAGTCACCCTCGACGGGCCGCCCTCCCGACTGTTGAGCA
qa	400	ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGl 4
8 8	6	TGTGCTCCCCTTCGTGGCAAGCTCTCTTTTGGGAGGCCGG 16
qq	42	srLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGl 440
λ	ŭ	TTCTGAT 17
qq	44	nriysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIl 460
λõ		GGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGG 17
QQ	460	SluAsnAlaAlaGlyHiBArgValAlaileSerThrTyrThrThrArgLeuGlyAlaGl 48
6	1770	GCGGCCCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGA 1
q	480	SerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGl 50
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Q Q		rPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu
δλ	1890	CGCTTTAGGCCTCCAG 1905
qa	520	gAlaLeuGlyLeuGln 525

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                                                                          GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC
                                                                                                                                                  CCGTCGCCCTGCCCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG
                                                                                                                                                                                                                                                SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr
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in vaccines
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95US-00542634.
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N-PSDB; AAT27112.
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Best Local Similarity:
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06-AUG-1996
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                                                                                    ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG
                                                                                                                                                                      LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer
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                                                                                                                                                                                                                                                                                                                                                                                                   A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with HEV peptide antigen, and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents a specifically claimed HEV peptide antigen. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 t correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                      - by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1057 CACTITACCGGCCTIAAIGGGGIAGGIGAAGICGGCCGCGGGAIAGCTCTAACAITACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT
                                                                                                                                                                                                                                                                                                                    Diagnosis of hepatitis E virus Burma and Mexico strain infection \mbox{immunoassay} with hepatitis E virus peptide antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-851-410A-10_COPY_5117_7096 (1-1980) x AAW35821 (1-327)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                  GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 37-40; 36pp; English
                                                                                                                                                                                                                                   Yarbough PO;
                            88US-00208997.
89US-00336672.
89US-00367486.
80US-00420921.
91US-00681078.
92US-00631335.
                                                                                                                                                                 92US-00876941
94US-00240049
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                                                                                                                                                                                                                                                                                    N-PSDB; AAT96966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                           11-APR-1989;
16-JUN-1989;
13-OCT-1989;
05-APR-1990;
05-APR-1991;
 09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                 01-MAY-1992
                               17-JUN-1988
                                                                                                                               17-JAN-1992
                                                                                                                                                   20-APR-1992
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                                                                                                                                                                                                                                   ram AW,
                                                                                                                                                                                                  (GENE-)
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DB:
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Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation.
                                                                                                   This sequence represents a Hepatitis E viral hollow particle protein described as ORF2. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptide and nucleic acid allow more accurate detection of HEV than previously possible
                           AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer
                                                                                     CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG
                                                                                                                                                                                                                                                                                                                                                Hollow particle protein; virus; antibody; detection; immunoassay;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                     Hepatitis E virus hollow particle protein ORF2
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/label= ORF2
/note= "partial sequence"
                                                                                                                                             927
                                                                                                                                                             301 AspPheAlaLeuGluLeuGluPheArg 309
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(KOKU-) KOKURITSU YOBO BISEI KENKYUSHO
                                                                                                                                             GACTITGCCTTAGAGCTTGAGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                   AAW76367 standard; protein; 549
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                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis virus
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                                                                                                                                                                                                                                   The present invention relates to an isolated avian hepatitis E virus having the nucleic acid sequence shown in ABT05872. Vaccines against the virus are also described, and can be used for protecting an avian or mammalian species from viral infection or hepatitis-splenomegaly syndrome caused by the avian or mammalian HEV. The present sequence is a hepatitis E virus protein described in the exemplification of the invention
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309
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Mismatches:
Indels:
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Matches:
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 splenomegaly syndrome caused by the
                           Example 11; Fig 5; 95pp; English
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309.00
100.00%
100.00%
46.89%
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Query Match:
                                                                                                                                                            Sequence 659 AA;
                                                                                                                                                                                                                                 Percent Similarity:
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infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                          CCAGITAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCC
                                                                                                                                                                                                                                                                                                                                                 TTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACA
                                                                                                                                                                                                                                                                                                                                                              244 LeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr
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                                                                                                                                                                                                                                                           GGCTATGCTATATCCATTTCTTGGCCTCAAACAACAACCACACCCTACATCTGTTGAC
                                                                                                                                                                                                                                                                       GlyTyrAlaileSerileSerPheTrpProGlnThrThrThrThrProThrSerValAsp
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                                                                                                                                                                                                               CAGTACCGGGTTGCCCGCCTACTATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGA
                                                                                                                                            US-09-851-410A-10_COPY_5117_7096 (1-1980) x AAR70323 (1-660)
                                                                          Matches:
Conservative:
Mismatches:
                                                                                                              Indels:
                                                                   Length:
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                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus.
                                 Sequence 660 AA;
                                                                                       Percent Similarity
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                                                       Alignment Scores:
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           LeuProLeuGlnAspGlyThrAsnThrHis1leMetAlaThrGluAlaSerAsnTyrAla
                                                                                                   LeuvalileProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr
                                                                                      GGCTATGCTATATCCATTTCTTTCTGGCCTCAAACAACCACAACCCTACATCTGTTGAC
                                                                                                                                                                           TTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACA
                                                                                                                                                                                                                      TCTGGTGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCT
                                         CAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGA
                                                       GlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigens of hepatitis E virus (HEV) - selectively immuno:reactive convalescent and/or acute phase circulating antibodies to HEV.
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                                                                                                                                                                                                                                          The present sequence is the protein prod, of ORF-2 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistara. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. 1gG or 1gM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. Daculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781
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                                                                                                            Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible
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                                                                                    Hollow particle protein; virus; antibody; detection; immunoassay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immuno-assays and nucleic acid hybridisation
                                       Hepatitis E virus hollow particle protein
                                                                                                                                                                                                                                                                                                                                                                                                   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 24-26; 29pp; Japanese
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                                                                                                                                                        Hepatitis virus.
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Search completed: August 16, 2004, 13:48:11 Job time : 114.682 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	8 1.2 153 2 8 1.2 172 2 8 1.2 177 2	
OM nucleic - protein search, using frame_plus_n2p model	8 1.2 205 2 T14744 8 1.2 22 2 H96711 6 1 3 33 3 373.63	
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Title: US-09-851-410A-10_COPY_5117_7096 Perfect score: 659 Sequence: 1 ATGCGCCTAGGCCTCTTTGTAAAACTCGGGAGTTGTAG 1980	25 8 1.2 254 1 IRWN31 26 8 1.2 266 2 H83564 27 8 1.2 267 2 A90252 28 8 1.2 267 2 T22978	
Scoring table: OLIGO Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 7.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	30 8 1.2 273 2 746639 hypothetical protes 31 8 1.2 292 2 7470313 cobalamin synthesis c 32 8 1.2 296 2 83664 00000000000000000000000000000000000	
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Command line parameters: -MODEL=frame+ n2p.model -DEV=xlp -MODEL=frame+ n2p.model -DEV=xlp -MODEL=frame+ n2p.model -DEV=xlp -MODEL=frame+ n2p.model -DEV=xlp -DB=PIR 76 -QFWT=fastan -SUFFIX=011: rpr -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0 -DWITS=Dits -START=1 -END=-1 -MARTIX=0.1150 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -UNITS=Dits -START=1 -DEV=XNALEN=0 -MAXLEN=2000000000 -USRR=USO9851410 @CGN 1 1.101 @runat 16082004 125717 9653 -NCPU=6 -ICPU=3 -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -USRR=USO9851410 @CGN 1 1.101 @runat 16082004 125717 9653 -NCPU=6 -ICPU=3 -NORM=EXT -HEAPSUZE=500 -MINLEN=200-MINLEN=2	ALIGNMENTS  - hepatitis E virus (strain Mexico)  evision 17-Feb-1994 #text_change 23-Jul-1999  andez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.	Tam, A
Database : PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir3:*	d sequencing of the Mexico isolate of hepatitis UID:93079857; PMID:1448913 ; NID:9330017; PIDN:AAA45732.1; PID:9330020	E virus (HE)
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	C;Superiamily: hepailitis E virus structural protein 2 C;Keywords: structural protein F;1-22/Domain: signal sequence #status predicted <sig> F;23-659/Product: structural protein 2 #status predicted <sp2></sp2></sig>	
Result Query No. Score Match Length DB ID Description	Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Dear Total Similarity:  Alignment Standarity:  Dear Total Similarity:  Dear Total	
659 100.0 659 1 B44212 120 18.2 660 1 VHWH2 109 16.5 123 1 C44212	Match: 100.00% Indels: 100.00% Gaps:	
.3 123 1 VANWARE SCIUCULAI .0 41 266 2 T36459 STOCHELL .4 325 2 G69580 acetyl-CoP .2 41 2 H58208 protamine	OS-03-631-410A-10_COFF_3111/096 (I-1980)	
8 1.2 74 2 519708 nypothetical hypothetical 8 1.2 104 2 C90345 hypothetical hypothetical 8 1.2 142 2 D75495 hypothetical	Qy         61         CCGACCGGTCAGCCGTCTGGCCGCCGCGCGCGCGCGCGCG	
8 1.2 142 2 JQ18 8 1.2 152 2 A461	Qy 121 ITCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	

qa		Db 401 ValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGln 420
oy Op	181 CCCTTTGCCCCAGACGTTGCCGCTGCGGGTCTGGACCTCGCCTTCGCCAACCACC 240	421 AspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln
Qy Pp	241 GGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGCGCCCCTCCGCTGCCTCCGTGGC 300	
QY Ph	301 CGACCTGCCACAGCGGGGGCTGCGGCTGACGGCTGTGGCGCCTGCCCATGACACCTCA 360	Oy 1381 ITTTCTGTTCTCCGAGCAATGANGTACTTTGGCTGCCCCCACTGCAGCGTATGAC 1440
r vo	CCCTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT CCCTTCCCGGACGTTGATTCTTCGCGGTGCAATTCTACTCTCCCGCGCCAGTATAATTTGTCTACT PCOVAIPTCASPVAIASPSerArgGlyAlaileLeuArgArgGlnTyrAsmLeuSerThr	1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
ςς Qα	421 TCACCCCTGACATCCTCTGTGGCCTCTGGCACTTTAGTCCTGTATGCAGCCCCCCTT 480	1501 AANGTIGGGACTGGCGGGGGCGGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTC
Qy	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540 	Oy 1561 GACGGCCGCCTCCCGACTGTTGACCAATATTCCAAGACATTCTTTGTGCTCCCCTT 1620
QY		1621 CGTGGCAAGCTCTCTTTTGGAGGCCGCACAAAAGCAGGTTATCCTTATAATTAT
ζζ	601 GCAGTTGGAGGCTATGCTATATCCATTCTTCTGGCCTCAAACCACCACACCCCTACA 660 	Oy 1681 AATACTACTAGTQACCAGATTCTCATTGAAAATGCTGCCGGCCATT 7740 
δ d	TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA	OY 1741 TCAACCTATACCACGGGCTGGGGCCGGTCGCGTCGCCATTTCTGCGGCCGCGGGTTTTG 1800  Db 581 SerThrTyrThrThrArgLeuGlyAladlyProValAlaIleSerAlaAlaAlaAlaUeu 600
Q Q	GCATCTGAATTGGTCATCCCAAGGGGCCCTTCATCATCGTGGTGGGTTGGCTTGGCTCG	Qy 1801 GCTCCACGCTCCGCCCTGGCTCTGCAGGATACTTTTGATTATCCGGGGCGGCGCAC 1860 
3 & E	AUGCLISTERCUTTICTION TO THE BEAUTY OF THE BE	Qy 1861 ACATITCANGACTICTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG 1920
G & A	CATGGCTCTCCAGTTAACTCCTATACCCCTTTATACCGGTGCCTTGCTGCTTACTG	Oy 1921 TCAACTGTCGCTCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1977
Qy Pp		RESULT 2 VHWH2 Structural protein 2 precursor - hepatitis E virus (strain Burma) C;Species: hepatitis E virus
oy da	961 TCCGGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG 1020 	C.Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999 C;Accession: C40779 M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.F Virology 185, 120-131, 1991
yo da	1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 	A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi A;Reference number: A40778; MUID:92024067; PMID:1926770 A;Accession: C40778 A;Molecule type: genomic RNA
<u>ک</u> و	1081 GGTGAAGTCGGCGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGC 1140 	A; Residues: 1-660 <tam> A; Rossidues: 1-660 <tam> A; Cross-references: GB:M73218; NID:g330023; FIDN:AAA45736.1; PID:g330026 A; Note: the authors translated the codon CGC for residue 2 as Ala C; Superfamily: hepatitis E virus structural protein 2</tam></tam>
Qy Db	1141 GGGCTCCCGACAGAATTAATTTCGTCGGCGGCAACTGTTTTATTCCGCCCGGTT 1200 	C;Keywords: structural protein F;1-22/Domain: signal sequence #status predicted <sig> F;23-660/Product: structural protein 2 #status predicted <sp2></sp2></sig>
, <b>φ</b>	GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG	Alignment Scores: 3.21e-112 Length: 660 Pred. No.: 120.00 Matches: 120

Oy 242 GGCCACTTGGCTCCACTTGGCCAGATCAGGCCCAGGCCCCTCGCTGCCTCCGCTGCCC 301  Db 95 GlyHisLeuAlaProLeuGlyGlulleArgProSerAlaProProLeuBroProValAla 114  Oy 302 GACCTGCCACAGCCGGGCTGCGGCGC 328  Il5 AspLeuBroGlnProGlyGlulleArgProSerAlaProProLeuBroProValAla 114  Oy 302 GACCTGCCACAGCCGGGCTGCGGCGC 328  RESULT 4  VHWWHE  structural protein 1 - hepatitis E virus (strain Burma) C;Species: hepatitis E virus C;Accession: Bdy778; Ad0736  A;Title: Hepatitis E virus C;Accession: Bdy778; Ad0778; August C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.F. A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vir A;Reference number: A40778; MUID:92024067; PMID:1926770  A;References GE: A virus (HEV): molecular cloning and sequencing of the full-length vir A;References GE: A; Manivell, V.; Ray, R. A;Residue: 1-123 crAM. A;Crossion: Bqy189; 1323 crAM. A;Crossion: Ad0736; MUID:92295577; PMID:1534953 A;Title: Indian hepatitis E virus shows a major deletion in the small open reading frame. A;Residual brye: genomic RNA A;Roccession: A40236; MUID:92295577; PMID:1534953 A;Residual bepatitis E virus shows a major deletion in the purple companie RNA A;Residual bepatitis E virus shows a major deletion in the purple companies to the patitis E virus shows a major deletion in the purple companies to the patitis E virus structural protein 1 C;Keywords: structural protein	ignment Scores:  1.9e-52	Oy 62 CGACCGGTCGGCGCGCGCGCGGCGGCGCGCGCGCGGCGGGGGG
Description   100.004   Missacches   0   0   0   0   0   0   0   0   0	structural protein 1 - hepatitis E virus (strain Mexico) C;Bpecies: hepatitis E virus C;Bpecies: hepatitis E virus C;Bate: 17-Fb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999 C;Accession: C44212 R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W. Virology 191, 550-558, 1992 A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HH A;Reference number: A44212; MUID:93079857; PMID:1448913 A;Accession: C44212 A;Molecule type: genomic RNA A;Residues: 1-123 cHUA> A;Across-references: G8:NW4506; NID:9330017; PIDN:AAA45731.1; PID:9330019 C;Superfamily: hepatitis E virus structural protein C;Keywords: structural protein	Alignment Scores: Pred. No.: Score: Score: 109.00 Matches: 109 Percent Similarity: 100.00\$ Mismatches: 0 Query Match: 15.54* Mismatches: 0 Query Match: 16.54* Mismatches: 0 Query Match: 16.54* Mismatches: 0 Cuery Match: 16.64* Mismatches: 0 Cuery Match: 16.64* Mismatches: 0 Cuery Matches: 16.64* Mismatches: 0 Cuery Matches: 16.64* Mismatches: 16.64* Mismatches

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R.Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, D. A. Biol. Chem. 271, 23547-23557, 1996
A.Title: Protamines of reptiles,
A.Reference number: A58208; MUID:96394458; PMID:8798564
  A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14880.1; PID:g2635385
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cypecies: Herpetosiphon aurantiacus
Cypecies: Herpetosiphon aurantiacus
Cypecies: Herpetosiphon aurantiacus
Cypacesion: 139708
Cyfacesion: 19708
Ryfacesion: 19708
Ryfacesion: 202, 1247-1256, 1991
Ryfitle: Cloning and molecular characterization of the HgiCI restriction/ modification Ayreference number: S19706; MUID:92111503; PMID:1662609
Ayresion: S19708
Ayresion: Displainary
Ayresidues: DNA
Ayresidues: 1-74 <RRO>
Ayresidues: 1-74 <RRO>
Ayresidues: EMBL:X55138
                                                                                                                                                                                                                                                                                                                                                        C.Species: Elaphe obsoleta quadrivittata
C.Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 07-May-1999
C.Accession: H58208
                                                                           A;Pathway: fatty acid biosynthesis
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C;Keywords: fatty acid biosynthesis; ligase
                                                                                                                                                                                                                                      US-09-851-410A-10\_COPY\_5117\_7096 (1-1980) x G69580 (1-325)
                                                                                                                                          925
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A,Molecule type: protein
A,Residues: 1-41 <HUN>
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                                     CysAlaLeuGlyLeuPheCysCysCysSerSerCysPhe 27
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C; Keywords: structural protein
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A;Residues: 1-142 <WHI>
A;Cross-references: GB:AE001921; GB:AE000513; NID:g6458330; PIDN:AAF10219.1; PID:g6458341
A;Experimental source: strain R1
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                                                                                                  hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: D75495
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pX-rex-orf I (alternatively spliced) - human T-cell lymphotropic virus type 1 C; Species: human T-cell lymphotropic virus type 1, HTLV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical 15.1K protein - bovine adenovirus 3 C;Species: Mastadenovirus bos3 (bovine adenovirus 3) C;Species: Mastadenovirus bos3 (bovine adenovirus 3) C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999 C;Accession: JQ1865 R;Mittal, S.K.; Prevec, L.; Babiuk, L.A.; Graham, F.L. J. Gen. Virol. 73, 3295-33100, 1992 A;Ritle: Sequence analysis of bovine adenovirus type 3 early region 3 and fine A;Reference number: PQ0499; MUID:93107871; PMID:1469367
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR0638
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              16 LeuThrLeuLeuThrArgSerSer 23
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A;Experimental source: strain WBR-1
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                               hypothetical protein 1 (px region) - human T-cell lymphotropic virus type 1 (isolate HAM Cispecies: human T-cell lymphotropic virus type 1, HTLV-1 C;Date: 28-0ct-1994 #sequence_revision 28-0ct-1994 #text_change 08-0ct-1999 C;Accession: C61547
R;Tsujimoto, A.; Teruuchi, T.; Imamura, J.; Shimotohno, K.; Miyoshi, I.; Miwa, M. AhOL Biol. Med. 5, 29-42, 1988 A;Title: Nucleotide sequence analysis of a provirus derived from HTLV-1-associated myelc A;Reference number: A61547; MUID:88232270; PMID:2897612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: C90345
R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE006641; NID: 913815078; PIDN: AAK42018.1; GSPDB: GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-99 <TSU>
A,Cross-references: GB:M37301; NID:g541634; PIDN:AAA45390.1; PID:g541637
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A; Residues: 1-104 < KUR>
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RESULT 15
D87322
hypothestical protein CC0590 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87322
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-411, 2001
A;Tile: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Retsius: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <STO>
A;Cenetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C; Date: 22-Sep-1893 #sequence_revision 18-Nov-1894 #text_change 17-Nov-2000
C; Accession: A46181; B46181
F; Koralnik, I.J.; Gessain, A.; Klotman, M.E.; Lo Monico, A.; Berneman, Z.N.; Franchini, Proc. Natl. Acad. Sci. U.S., 89, 8813-8817, 1992
A; Title: Protein isoforms encoded by the pX region of human T-cell leukemia/lymphotropic A; Reference number: A46181
A; Molecule type: nucleic acid A; Molecule type: nucleic acid A; Resquence extracted from NCBI backbone (NCBIP:114304)
A; Accession: B46181
A; Boldminary; not compared with conceptual translation A; Accession: B46181
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P51371 P74638 Q54766

Q9wu40

Q9rnn5 Q9gm70 Q9czc8 P78589

Q04073 P10896 Q9a649

Q13064 Q92459 Q29499

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93079857; PubMed=1448913;
Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,
Bradley D.W., Tam A.W., Reyes G.R.;
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E virus (HEV).";
Virology 191:550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
STRUCTURAL PROTEIN 2.
CF75E75EFD8FBE2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis E virus (etrain Mexico) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                              003500;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0FBB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor.
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RAA3_CHLRE
HRX_HUMAN
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ACES_RABIT
ACES_HUMAN
                                                                                                                                                                     ACES RAT
PSAB CYAME
DUR3 YEAST
T2D4 HUMAN
CHS2 EXODE
YEGN ECOLI
                                                                    K193_MOUSE
FDFT_CANAL
OAPT_PSEPU
P3A2_STRPU
RCA_ARATH
EX7L_CAUCR
MKR3_HUMAN
       ACCA_PORPU
ACCA_SYNY3
ACCA_SYNP7
MAN1_MOUSE
DGT1_ZYMMO
S17A_RABIT
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MEL APIDO
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InterPro; IRR004451; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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STANDARD;
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VST2_HEVME
ID _VST2_HEVME
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Q044612 hepatitis e
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Q08xh7 clostridium
P06498 human adeno
P28270 herpes simp
P51249 porphyra pu
P29786 aedes aegyp
Q09952 caenorhabdi
Q9fuz2 arabidopsis
P46316 antithamnio
                                                                                (without alignments)
11307.070 Million cell updates/sec
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                                                                                                                                 ATGCGCCCTAGGCCTCTTT.....GTAAAACTCGGGAGTTGTAG 1980
                                                                     August 16, 2004, 13:36:13 ; Search time 18.2362 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                   using frame_plus_n2p model
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UL03_HSV2H
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TRY3_AEDAE
YSR4_CAEEL
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Q15542 P30601 P76398 Q10900

P33413

Oy 961 TCCCGTTACTCCAGCACTGCTCGCCCGAGGGGCCGACGGGACTGCGGAGCTG 1020	Oy 1141 GGCTCCCGACAGAATTACTTCGTCGGCGGGCAACTGTTTTATTCCCGCCCG	Qy         1321 GATTATGACAACCAGCATCGGCCCACCCCGTCGCGCCATCTCGGCCT 1380           bb         441 AspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPro 460           Qy         1381 TTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGCCCTCACTGCAGCCGAGTATGAC 1440           Db         461 PheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAsp 480           Qy         1441 CAGTCCACTTACGGCTCACACTGCAGCTGAGTTTATATCTCGGACGTGACTTTGGTG 1500           Qy         1441 CAGTCCACTTACGGCTCACACTCACCTCGACCGGTGACTTTGGTG 1500           Db         481 GlnSerThrTyrGly8erSerThrGlyProValTyrIleuVal 500	Qy         1501 AATGTTGCGACTGGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTC 1560           Db         501 AsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeu 520           Qy         1561 GACGGCGCCTCCCCGACTGTTGAGCAATATTCCAAGACATTCTTGTGCTCCCCTT 1620           Db         521 AspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhebheValLeuProLeu 540           Qy         1621 GGTGCCAGCTCTCTTTGGCGCGCACAACAACAAAGCAGTTATCCTTATAATTAT 1680           Qy         1621 GGTGCCAGCTCTCTTTGGCGCGCACAACAACAAAGCAGTTATCCTTATAATTAT 1680           Db         541 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlYTyrProTyrAsnTyr 560	Qy         1681 AATACTACTGCTGGATTCTGATTGAAAATGCTGCGGCCATCGGGTCGCCATT 1740	F 60
Alignment Scores:  Pred. No.:  Pred. No.:  Score:  Score:  G59.00 Matches:  Fercent Similarity:  100.00\$ Mismatches:  Query Match:  100.00\$ Mismatches:  Gaps:  US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVME (1-659)  Oy	61 CCGACCGGTCGGCGCGCGCGGGGGGGGGGGGGGGGGGGG	241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGGGCCCCTCCGCTGCCTCCGTCGCTGCCTCCGTCGCTCCGTCGCTGCCTCCGTCGCTCGCTCCGTCGCTCCGTCGCTCGTCG	TroAspValAspSerArgGlyAlalleLeuArgArgGinTyrAsnLeuGrapargGinTyrAsnLeuGrapargGlnTyrAsnLeuGrapargGlnTyrAsnLeuGrapargGlnTyrAsnLeuGrapargGCGCGGCGCGCGCGCGCGGGACTAATTAGTCCTGTATGCCGCGGGGTACTAATACTCACATTATGGCCACAGAGTACTGCGCGCGC	601 GCAGTTGGAGGCTATGCTTTTCTTGCCCTCAAACAACCACCACCACAACCACCCTACA 6 [	241 AtaSerGluLeuValIleProSerGluArgleuHisTyrArgAsnGlnGlyTrpArgSer 260  Qy 781 GTTGAGACATCTGGTGTTGCTGAGGAGCCACCTCCGGTCTTGTCATGTATGCATA 840  261 ValGluThrSerGlyValAlaGluGluAlaThrSerGlyLeuValMetLeuCysile 280  Qy 841 CATGGCTCTCCAGTTAACTCCTATACCAATACCGGTGCCCTTGGCTTACTG 900

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910 TTAGAGCTTGAGTTTCGCAATCTCACC
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                                                                                                               MEDLINE=92115700; PubMed=1731327;
TSATEV S.A., EMETSON S.U., Reyes G.R., TSATEVA T.S., Legters L.J.,
MAIN I.A., Idbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:559-563 [1992].
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
                                                                                                                                                                                                BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVPA (1-660)
                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURAL PROTEIN 2.
8085BC53CFB46FD3 CRC64;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Heperitis E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Hepatitis B-like viruses.
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Matches:
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InterPro; IPR008975; Viral_cap_coat.
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Signal.
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660 AA;
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                                                                               NCBI_TaxID=33774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92261377; PubWed-1584074;
Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno K.,
Win K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVRH (1-485)
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                                                                                                                                                                                                                                                                                 Hepatitis E virus (isolate Rhesus) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Matches:
Conservative:
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
Structural protein 2 (Fragment).
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304 LeuGluLeuGluPheArgAsnLeuThr 312
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InterPro; IPR008975; Viral_cap_coat.
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                                                                                                                                                         289 ThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPhe 308
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                              805 GAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length viral genome.";
Virology 185:120-131(1991).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDIJNE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVBU (1-660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
STRUCTURAL PROTEIN 2.
5832A013CCC4A61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-PEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Burma) (HEV).
Viruses; ssRAA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                     660 AA
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M73218; AAA45736.1; -.
PIR; C40778; VIKWH2.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PP03014; SP2; 1.
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70978 MW;
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100.00%
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18.21%
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                                                                                                                                                                                                                                                      309 ArgAsnLeuThr 312
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Best Local Similari
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P29326;
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                                                                                                                             865
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SIGNAL
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684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 SerThrAspValArgIleLeuValGInProGlyIleAlaSerGluLeuValIleProSer 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 GAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAG 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
"Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virus Genes 7:95-109(1993).
-!- FUNCTION: CONTENIS A HICH BASIC AMINO ACID CONTENT SUGGESTING
-!- FUNCTION: CONTENIS A HICH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Myanmar) (HEV).
Hepatitis E-like viruses.
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Matches:
Conservative:
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STRUCTURAL PROTEIN
3A82A4EA255C6253
                                                                                                                                                                                                                          660 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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660
70998 MW;
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                                                                           CGCAATCTCACC 936
                                                                                                                        177 ArgAsnLeuThr 180
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23 (
660 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31769;
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Best Local Similarit
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Pred. No.:
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                                                                                                                                                                                                                                               004611;
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  GlyHisLeuAlaProLeuGlyGluIleArgProSerAlaProProLeuProProValAla 114
   15 CysAlaLeuGlyLeuPheCysCysCysSerSerCysPheCysLeuCysCysProArgHis 34
CCTTTGCCCCAGACGTTGCCGCTGCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCCC
   2 TGCGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTGTTTCTGCCTATGTTGCCCGCGCCCAC
   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J., Malik I.A., Igbal M., Purcell R.H.; "Characterization of a prototype strain of hepatitis E virus."; Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
  "Hepatitis E virus (HEV): molecular cloning and sequencing of
  STRAIN=Burma;
MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.,
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVBU (1-123)
   EMBL; M80581; AAA45726.1; -.
PIR; B40778; VHWWHE.
INCEPPO; IPRO03384; HEV_ORF2.
Pfam; PFC444; HEV_ORF2; 1.
SEQUENCE 123 AA; 12676 WW; 8A5A798B1B74EDE5 CRC64;
   stage;
  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 1 (ORF3).
Hepatitis E virus (strain Burma) (HEV), and
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; seRNA positive-strand viruses, no DNA sta
Hepatitis E-like viruses.
   Length:
Matches:
Conservative:
   Mismatches:
  123 AA.
  Indels:
  or send an email to license@isb-sib.ch).
  GACCTGCCACAGCCGGGGCTGCGGCGC
   MEDLINE=92115700; PubMed=1731327;
  EMBL; M73218; AAA45735.1; -.
  1.06e-51
61.00
100.00%
100.00%
9.26%
  full-length viral genome."
Virology 185:120-131(1991)
  STANDARD;
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  Best Local Similarity:
  STRAIN=Pakistan;
  Percent Similarity:
   Alignment Scores:
  VST1_HEVBU
P29325;
   75
   95
  242
  302
   Query Match:
  Pred. No.:
   RESULT
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  729
   789
  244 LeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr 263
   849
   223
   61
   54
  SerGlyValThrGlyLeulleLeuSerProSerGlnSerProllePhelleGlnProThr 74
  15 CysAlaLeuGlyLeuPheCysCysCysSerSerCysPheCysLeuCysCysProArgHis 34
   35 ArgProvalSerArgLeuAlaAlaValValGlyGlyAlaAlaAlaValProAlaValVal
                                     GlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSerValAsp
   GGCTATGCTATACCATTTCTTGTGGCCTCAAACAACCACAACCCCTACATCTGTTGAC
   TTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACA
   TCTGGTGTTGCTGAGGAAGGCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCT
  Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,
Bradley D.W., Tam A.W., Reyes G.R.;
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
  US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVME (1-123)
  PIR; C44212; C44212.
InterPro; IPR003384; HEV ORF2.
Pfam; PF02444; HEV ORF2; SEQUENCE 123 AA; 12714 WW, C888F5D638852A68 CRC64;
   Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
   Length:
Matches:
Conservative:
Mismatches:
   01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
  123 AA
   Indels:
  (HEV)
   Hepatitis E virus (strain Mexico)
  SEQUENCE FROM N.A.
MEDLINE=93079857; PubMed=1448913;
  EMBL; M74506; AAA45731.1; -.
   2.1e-99
109.00
100.00%
100.00%
  Virology 191:550-558(1992).
  STANDARD;
  Structural protein 1
   Best Local Similarity:
  NCBL_TaxID=31768;
   virus (HEV).
   Percent Similarity:
  Alignment Scores:
  HEVME
  122
   N
   730
   790
  62
   Query Match:
  VST1_HEVME
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AC 0043H
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10-OCT-2003 (Rel. 42, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
   subtilis
    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
  181
  GTCAGCCGTCTGGCCGCCGTCGTGGGCGGCGCAGCGCGGTACCGGCGGTGGTTTCTGGG 127
  74
                        54
  55 SerGlyValThrGlyLeuIleLeuSerProSerGlnSerProIlePheIleGlnProThr
   "Sequence and gene structure of the hepatitis E virus isolated from
  MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVMY (1-123)
  EMBL; D10330; BAA01173.1; -,
InterPro; IPR003384; HEV_ORF2.
Pfam; PF02444; HEV_ORF2; 1.
SEQUENCE 123 AA; 12751 MW; FB81143F0B31F8A4 CRC64;
   01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
Structural protein 1 (ORF3).
Hepatitis B virus (strain Myanmar) (HEV).
Viruses; ssNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
   123
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   Conservative:
   Mismatches:
   123 AA.
   325 AA
   (Rel. 36, Created)
(Rel. 36, Last sequence update)
   Length:
   Indels:
   Virus Genes 7:95-109(1993).
   1.03e-49
   59.00
100.00$
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8.95$
   STANDARD;
   STANDARD;
  SEQUENCE FROM N.A.
   Best Local Similarity:
  182 CCT 184
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   Percent Similarity:
   01-OCT-1993
   Alignment Scores:
   VST1_HEVMY
Q04612;
   15-JUL-1998
15-JUL-1998
   ACCA BACSU
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischi C.V., Collagell B., Capuano V., Daniel R.A.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Pujita Y., Fume S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Cobyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oddega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sckiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tacconi E., Takagi T., Takahashi H., Takemari K.,
RA Takadia N., Wanbutet R., Wedler E., Wedler F., Vasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto H., Vamane K., Yoshikawa H.F., Zammere B., Yoshikawa H.F., Zammere M., Yoshikawa H.F., Zammere M., The Complete genome sequence of the Gram-positive bacterium Bacillus
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  -i- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA (By similarity).

-:- CATALYTIC ACTIVITY: Carboxybiotin carboxyl carrier protein + machyl-CoA.

-:- PATHMAY: Long-chain carboxyl carrier protein + malonyl-CoA.

-:- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
   CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY). SIMILARITY: TO THE C-TERMINUS OF MAMMALIAN PROPIONYL-COA
   Lapidus A., Galleron N., Sorokin A., Ehrlich S.D., "Sequencing and functional annotation of the Bacillus subtilis genes
   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
  MEDLINE=98044033; PubMed=9384377;
   MEDLINE=98048467; PubMed=9387221;
  in the 200 kb rrnB-dnaB region.";
Microbiology 143:3431-3441(1997).
   EMBL; AF008220; AAC00341.1; -. EMBL; Z99118; CAB14880.1; -.
  CARBOXYLASE BETA CHAIN.
   Nature 390:249-256(1997)
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   Bacillus subtilis
ACCA OR BSU29200
   NCBI_TaxID=1423;
```

```
SEQUENCE FROM N.A.
   NCBI_TaxID=28285;
   COMPLETE GENOME.
   PHOSPHORYLATION.
   O-GLYCOSYLATION
  phosphoserine
   E315_ADE05
  by TNF
  83
   P06498;
Query Match:
  RESULT
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   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (89 similarity).
   STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shimizu T., Ogasawara N., Hartori M., Kuhara S., Hayashi H.,
"Complete genome sequence of Clostridium perfringens, an anaerobic
  -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
  Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
  US-09-851-410A-10_COPY_5117_7096 (1-1980) x ACCA_BACSU (1-325)
              Subtilist; BG12557; accA.
InterPro; IPR001095; Ac-CoA_carboxylA.
Pfan; PF03255; ACCA; 1.
PRINTS; PR01069; ACCCTRFRASEA.
TIGRFMAS; TIGR00513; accA; 1.
Fatry acid biosynthesis; Ligase; Complete proteome.
SEQUENCE 325 AA; 36333 MW; 9B177DEE4A5B5864 CRC64;
  protein; Complete proteome.
121 AA; 12535 MW; 5AF9F83D2C94AC3E CRC64;
   Length:
Matches:
Conservative:
Mismatches:
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPLL OR CPE2414.
  121 AA.
  Indels:
   294 GGAGGCAGCGGAGGGGCCTGGCCTG 268
   199 GlyGlySerGlyGlyAlaLeuGlyLeu 207
   Gaps:
   HAMAP, MF 00368, -, 1.

InterPro; IPR008932; Ribos L12/7 olig.
InterPro; IPR000206; Ribosomal L12.
PFam, PF00542; Ribosomal L12; 1.

ProDom; PD001326; Ribosomal L12; 1.

IIGREAMS; TIGR00855; L12; 1.
  proteome
  PRT;
  EMBL; AP003194; BAB82120.1; -.
  100.00%
100.00%
1.40%
   4.42
  STANDARD;
PIR; G69580; G69580.
  SEQUENCE FROM N.A.
  Best Local Similarity:
   NCBI_TaxID=1502;
   flesh-eater.";
   Percent Similarity:
   Alignment Scores:
  Alignment Scores:
  Clostridium
  RL7 CLOPE
  Ribosomal
  SEQUENCE
  08XHR7;
  Query Match:
   RESULT 10
  CLOPE
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Length: Matches:

Conservative: Mismatches:

8.00 100.00% 100.00%

> Percent Similarity: Best Local Similarity:

50.1

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
  MEDLINE=90177214; PubMed=2309441;
Tollefson A.B., Krajcsi P., Pursley M.H., Gooding L.R., Wold W.S.M.;
"A 14,500 M protein is coded by region E3 of group C human
adenoviruses.";
   MEDLINE-92188523; PubMed=1532104; Krafosi V. Wold W.S.M.; Wold W.S.M.; "The adenovirus E3-14-5K protein which is required for prevention of TNF cytolysis and for down-regulation of the EGF receptor contains
   -!- FUNCTION: Down-regulates the EGF receptor and prevents cytolysis
   MEDLINE=92263760; PubMed=1533979;
Krajcsi P., Tollefson A.E., Wold W.S.M.;
"The E3-14.5K integral membrane protein of adenovirus that is required for down-regulation of the EGF receptor and for prevention of The Tree Tree and For prevention of the Partolysis is 0-919cosylated but not N-glycosylated."; Virology 188:570-579(1992).
  Human adenovirus type 5.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
  Chroboczek J., Bieber F., Jacrot B.; "The sequence of the genome of adenovirus type 5 and its comparison
   MEDIJINE=92148953; PubMed=1531370; MEDIJINE=92148953; PubMed=1531370; MEDIJINE=92148953; PubMed=1531370; Medification in the sequence of the s
  MEDLINE-85092388; PubMed=2981456;
Cladaras C., Wold W.S.M.;
"DNA sequence of the early E3 transcription unit of adenovirus
Virology 140:28-43(1985).
  -!- ŠIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x RL7_CLOPE (1-121)
   -!- PTM: Phosphorylated on serine; O-glycosylated,
   01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
  132 AA.
Indels:
  with the genome of adenovirus type 2."; Virology 186:280-285(1992).
                                  Gaps:
  GCCGTCGTGGGCGCGCAGCGGCG 106
   Early E3B 14.6 kDa protein precursor.
  PRT;
  38 AlavalvalGlyGlyAlaAlaAla
   MEDLINE=92087470; PubMed=1727603;
   Virology 187:492-498(1992).
  IDENTIFICATION OF PROTEIN.
   Virology 175:19-29(1990).
  STANDARD;
  lated
  glycosy
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RR2 PORPU
P51249;
                          93
  Query Match:
   P28279
  Local
  Best
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  Eur. J. Biochem. 201:53-59(1991).
-!- FUNCTION: Increases water and sodium absorption in the intestine and gall-bladder.
-i- SIMILABAILY: Contains 1 SoHo domain.
PIR; S17837; S17837.
InterPro; IPR003127; Sorb.
Probom; PE02208; Sorb; 1.
SMART; SM0459; Sorb; 1.
   InterPro; IPR008131; Adeno B3 14 5.
Pfam; PF04834; Adeno E3 14 5; 1.
Early protein; Transmembrane; Glycoprotein; Phosphorylation; Signal.
  TISSUE-Intestine;
MEDLINE=92007891; PubMed=1915377;
MEDLINE=92007891; A., Pansu D., Joernvall H., Carlquist M., Guignard Jourdan G., Desvigne A., Collinet M., Caillet C., Mutt V.;
"Isolation and characterisation of porcine sorbin.";
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x E315_ADE05 (1-132)
   EARLY E3B 14.6 kDa PROTEIN
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x SORB_PIG (1-153)
   POTENTIAL.
524690C4AD9B9A74 CRC64;
  A49C219455BB1417 CRC64;
   132
0 0 0 0
   153
8
0
   Conservative:
Mismatches:
Indels:
   Matches:
Conservative:
Mismatches:
  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
   153 AA
  Length:
Matches:
   Length:
  Indels:
  Gaps:
  Gaps:
   1097 CCGCGGCCGACTTCACCTACCCCA 1074
   EMBL; M73260; -; NOT ANNOTATED_CDS.
EMBL; X03002; CAA26786.1; -.
   PRT;
   SOHO
  75 PC
14750 MW;
  46 S
AA; 17481 MW;
   49.5
8.00
100.00%
100.00%
1.24%
   48.5
8.00
100.00%
100.00%
1.24%
  PROSITE; PS50831; SOHO; 1.
   STANDARD;
   132
  51
132 AA;
   Percent Similarity:
Best Local Similarity:
  Best Local Similarity:
  Sus scrofa (Pig)
   19
  153
  Percent Similarity:
   Alignment Scores:
Pred. No.:
   Alignment Scores:
  TRANSMEM
SEQUENCE
  SEQUENCE
   SORB PIG
   SEQUENCE
  Sorbin.
   SIGNAL
  Query Match:
DB:
  Query Match:
  ..
No.:
  RESULT 12
SORB PIG
   Score:
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   PAGE STANDARD DE PAGE SON CONTRA SERVICE SON CONTRA
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119 CCACCGCCGGTACCGCCGCTGCGC 96

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   Chloroplast.
Eukaryota, Rhodophyta, Bangiophyceae, Bangiales, Bangiaceae, Porphyra.
NCBI_TaxID=2787,
  McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
"Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2.";
J. Gen. Virol. 72:3057-3075 (1991).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL3,
HSV-2 UL3, EHV-1 60, AND VZV 58.
   STRAIN=Avonport; Reith M.E., Munholland J.; Reith M.E., Munholland J.; Reith M.E., mucleotide sequence of the Porphyra purpurea chloroplast
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x UL03_HSV2H (1-233)
  InterPro; IPR005035; Herpes UL3.
Pfam; PF03369; Herpes UL3; 1.
SEQUENCE 233 AA; 25649 MW; B38F613BD839AA24 CRC64;
  Herpes simplex virus (type 2 / strain HG52).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
   233
8
0
  Length:
Matches:
Conservative:
Mismatches:
Indels:
   (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 24, Last annotation update)
   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S2.
    233 AA
  241 AA
   Gaps:
   421 TCACCCCTGACATCCTCTGTGGCC 444
   PRT;
  SEQUENCE FROM N.A. MEDLINE=92113549; PubMed=1662697;
  Alphaherpesvirinae; Simplexvirus
NCBI_TaxID=10315;
   EMBL; D10470; BAA01266.1; -.
  45.7
8.00
100.00%
100.00%
1.21%
STANDARD;
  STANDARD;
  PIR; JO1496; WMBEHK.
   SEQUENCE FROM N.A.
   Similarity:
  Porphyra purpurea.
   Percent Similarity:
   01-OCT-1996 (
01-OCT-1996 (
28-FEB-2003 (
Chloroplast 3
   Alignment Scores:
  01-DEC-1992
   01-DEC-1992
01-DEC-1992
   Protein UL3.
    UL03 HSV2H
   RR2_PORPU
ID _ RR2_F
AC PSI2_H
AC 01-0C
DT 01-0C
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8
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   two cDNA clones coding
   "Isolation, sequencing and characterization of two cDNA clones coding for trypsin-like enzymes from the midgut of Aedes aegypti."; Insect Mol. Biol. 2:71-79(1993).
- FUNCTION: Major function may be to aid in digestion of the blood
  -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
              Plant Mol. Biol. Rep. 13:333-335(1995).
-!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
   Eukaryotā; Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes.
  MEDLINE=97242546; PubMed=9087545;
Kalhok S., Tabak L.M., Prosser D.E., Brook W., Downer A.E.R.,
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x RR2_PORPU (1-241)
   FA17DA9C352FC866 CRC64;
   Length:
Matches:
Conservative:
Mismatches:
   -!- SUBCELLUIAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Midgut.
-!- SIMILARITY: Belongs to peptidase family Sl.
   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
   254 AA.
  Indels:
   HAMPS, MF 00291; -1.

InterPro; IPR001865; Ribosomal S2.
InterPro; IPR001865; Ribosomal S2.
InterPro; IPR001818; Ribosomal S2.

Pfam; PP00318; Ribosomal S2; 1.

PRINTS; PR00395; RIBOSOMĀLS2.

TIGRFAMS; TIGR01011; TDSB bact; 1.

PROSITE; PS00963; RIBOSOMĀLS2.

PROSITE; PS00963; RIBOSOMĀLS2.

Ribosomal protein; Chloroplast.

SEQUENCE 241 AA; 27198 MW; FA17DA9GC3
   or send an email to license@isb-sib.ch).
  1147 CCGACAGAATTAATTTCGTCGGCT 1170
  231 ProThrGluLeuIleSerSerAla 238
  Trypsin 3A1 precursor (EC 3.4.21.4). Aedes aegypti (Yellowfever mosquito)
   EMBL; U38804; AAC08135.1; -.
  100.00%
100.00%
1.21%
   45.5
   STANDARD;
  873170; 873170.
  SEQUENCE FROM N.A.
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Percent Similarity:
Rest Local Similarity:
   NCBI_TaxID=7159;
   Alignment Scores:
   White B.N.;
   IRY3 AEDAE
  Query Match:
DB:
  P29786;
   RESULT 15
TRY3_AEDAE
  Score:
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REQUIRED FOR SPECIFICITY (BY SIMILARITY).

43AAR13BBDE7D485 CRC64;
  (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x TRY3_AEDAE (1-254)
   PFERM; PP000089; Trypsin; 1.
PRINTS; PR00020; Trypsin; 1.
PROSITE; PS00020; Tryp SPC; 1.
PROSITE; PS00034; TRYPSIN DOM; 1.
PROSITE; PS000134; TRYPSIN HIS; PALSE_NEG.
PROSITE; PS010135; TRYPSIN SEE; 1.
Hydrolase; Serine protease; Signal; Zymogen; Digestion;
   POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN 3A1.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
  Conservative:
Mismatches:
  Matches:
  Length:
   Indels:
  1767 CGGTCCGGTCGCCATTTCTGCGGC 1790
   Search completed: August 16, 2004, 13:48:51
Job time : 26.2362 secs
   InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
  54
   47 ArgSerGlyArgHisPheCysGly
   26939 MW;
   100.00%
100.00%
1.21%
EMBL; X64362; CAA45714.1;
PIR; S19890; TRWV3Y.
   20
27
254
254
1113
2009
69
194
2229
                            HSSP; P00763; 1DPO.
MEROPS; S01.112; -.
  254 AA;
  Percent Similarity:
Best Local Similarity:
   21
28
68
1113
209
53
178
205
205
   Alignment Scores:
  ACT_SITE
ACT_SITE
  ACT_SITE
DISULFID
  DISULFID
   DISULFID
   SEQUENCE
   PROPEP
CHAIN
  Query Match:
   SIGNAL
   Pred. No.:
   Score:
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   16,
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  Sequence
  Sequence
   Sequence
   Sequence
  Sequence
   Sequence
   Sequence 16, Application US/08240049B

Batent No. 568629
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Tam, Albert W.
APPLICANT: Yarbough, Patrice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
   REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
  US-08-240-049B-14
US-08-259-148A-16
US-08-84-054-16
US-08-84-054-16
US-08-8-634-18
US-07-870-985A-18
US-07-870-985A-18
US-07-172-699-20
US-09-172-699-20
US-09-172-699-20
US-09-462-606-12
US-09-462-606-55
US-09-
   US-08-542-634-26
PCT-US95-13703-26
US-08-542-634-28
PCT-US95-13703-28
  PCT-US95-13703-15
  US-08-240-049B-15
  US-08-542-634-15
US-08-477-292-15
   SSEE: Genelabs Technologies, Inc. F: 505 Penobscot Drive Redwood City
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
  659 amino acids
USA
  94063
   ð
   US-08-240-049B-16
   CITY: ReSTATE: C
  LENGTH:
   4435
4435
3392
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   327
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  149
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   149
  RESULT 1
 -MODEL-frame+_n2p.model -DEV=xlp
-MODEL-frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPFTO spool_p/USO9851410/runat_16082004_125718_9682/app_query.fasta_1.4238
-Q=/cgn2_1/USPFTO spool_p/USO9851410/runat_16082004_125718_9682/app_query.fasta_1.4238
-DB=ISSUEd_Patents_AA -QFWT=fastan -SUFFIX=oli.rai_-MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCAMIGN=200 -THR_SCORE_aquality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-USFR=45 -DOCAMIGN=200 -THR_SCIRE=0 -MAXIEN=200000000
-USFR=45 -DOCAMIGN=200 -MINIEN=0 -MAXIEN=200000000
-USFR=45 -DOCAMIGN=200 -MINIEN=0 -MAXIEN=200000000
-USFR=45 -DOCAMIGN=200 -MINIEN=0 -MAXIEN=2000000000
-USFR=45 -DOCAMIGN=200 -THREADS=1 -XGAPEXT=60 -LONGLOG
-EGAPOXT=1 -YGAPOP=60 -YGAPEXT=60 -DELDXT=7
  (without alignments)
10229.686 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Sequence 20, Sequence 20, Sequence 14, Sequence 16, Sequence 116, Sequence 14, Sequence 18, Sequence 18, Sequence 18, Sequence 18,
  1 ATGCGCCCTAGGCCTCTTTT......GTAAAACTCGGGAGTTGTAG 1980
  Sequence 16,
  August 16, 2004, 13:41:04; Search time 19.9849 Seconds
   Description
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
  - protein search, using frame_plus_n2p model
   US-08-240-049B-16
US-08-259-148A-20
US-08-484-054-20
US-07-876-941A-20
US-08-477-292-14
US-07-870-985A-20
US-08-542-634-14
PCT-US95-13703-14
US-08-542-66-48
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                             APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Xrawczynski, Krzysztof Z.
APPLICANT: Xrawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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COMPATE: IBM PC compatible
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FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
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   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
  REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
   PRIOR DATE: 13-0CT-1989
PRIOR DATE: 13-0CT-1989
PRIOR APPLICATION DATA:
PRIOR DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
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RICH APPLICATION DATA:
APPLICATION NUMBER: US 208,997
  Sequence 20, Application US/08259148A Patent No. 5741490 GENERAL INFORMATION:
  FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INPORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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Daniel W.

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APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: APPLICANT: Mepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
  3: Dehlinger & Associates
350 Cambridge Avenue, Suite
   COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
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SOFTWARE: Patentin Release #1.0, Ve
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FILING DATE: 07-JUN-1995
Bradley, Daniel W.
Twu, Jr-Shin
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Tam, Albert W.
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CITY: Palo Alto
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Version #1.25

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FILING DATE: 13-OCTOBER-1989
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  FILING DATE: 16-UUNE-1989
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APPLICATION NUMBER: US 336,672
FILING DATE: 11-ARRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UUNE-1988
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
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FILING DATE: 17-JAN-1992
  APPLICATION NUMBER: US 367,486
   NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615
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  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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Sequence 20, Application US/08484054 Patent No. 5770669 GENERAL INFORMATION: APPLICANT: Reyes, Gregory R.

US-08-484-054-20

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 420,921
FILING DATE: 13-CTOBER-1989
PRIOR APPLICATION NUMBER: US 420,921
FILING DATE: 13-CTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UNDER: US 367,486
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  Length:
Matches:
Conservative:
Mismatches:
  ORF 2, MEXICO, FIGURE
   Indels:
Gaps:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUME-1988
ATTORNEY/AGENT INFORMATION:
  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INPORMATION:
TELEPAN: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
  659.00
100.00%
100.00%
   : 659 amino acids
amino acid
GY: linear
          STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
COMPUTER: IBM PC comp.
   MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
  INDIVIDUAL ISOLATE:
Palo Alto
   Percent Similarity:
Best Local Similarity:
  US-07-876-941A-20
  TOPOLOGY:
   Alignment Scores:
   LENGTH:
  19
  21
   121
   41
   181
   Query Match:
DB:
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CGACCTGCCACAGCCGGGGCTGCGGCGCTGACGGCTGTGGCGCCTGCCCATGACACCTCA 360
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ORF-2
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Conservative:
Mismatches:
  Indels:
   Length:
US/08/327,952
  NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REPERBENG-FOCKET NUMBER: 63.2P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)369-9500
TELEFAX: (415)369-0709
INFORMATION FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
   659.00
100.00%
100.00%
                                 ATTORNEY/AGENT INFORMATION:
   MOLECULE TYPE: protein HYPOTHETICAL: NO
APPLICATION NUMBER:
  INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
  linear
  Percent Similarity:
Best Local Similarity:
  ORIGINAL SOURCE:
                 FILING DATE:
   TYPE: ami:
TOPOLOGY:
   Alignment Scores:
Pred. No.:
   US-08-477-292-14
   421
   601
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  541 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyr 560
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  SerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu
   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.202
FILING DATE:
CLARGE DATE:
   Antigens
   APPLICANT: Fuerst, Thomas
APPLICANT: McAtee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E Virus Antige
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathleen M. Desjardins, M.D.
STREET: Redwood City
   Sequence 14, Application US/08477292 Patent No. 6291641 GENERAL INFORMATION:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  SD
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   -08-477-292-14
  COUNTRY:
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1861 ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTTCCAG 1920
                   TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTG 1800
  1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAACTCGGGAGTTG 1977
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   621 ThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGln
   APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.-Shin
APPLICANT: Twu, Jr.-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
   SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
  4600-0093.30
  3: Dehlinger & Associates
350 Cambridge Avenue, Suite
  PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 420,921
FILING APPLICATION DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UNR-1989
PRIOR APPLICATION DATE: US 35,672
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   Sequence 20, Application US/07870985A Patent No. 6455492 GENERAL INFORMATION:
   US 208,997
   REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
   20-APRIL-1992
   FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,
   FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
  Fabian, Gary R.
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   Palo Alto
  FILING DATE: 20
   USA
   ZIP: 94306
   RESULT 6
US-07-870-985A-20
  ADDRESSEE:
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   COUNTRY:
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Matches:
Conservative:
Mismatches:
Indels:
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  Gaps:
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659.00
100.00%
100.00%
 amino acids
LENGTH: 659 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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  Similarity
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Best Local Similari
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   Virus Antigens and Methods
  Hepatitis E virus (Mexico strain) r62kDa, FIGURE 4
   ννοοοο
4 4
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   NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE Cathleen M. Desjardins, M.D.
STREET: 505 Penobscot Drive
CITY: Redwood City
STRATE: CA
COUNTRY: US
ZIP: 94603
ZIP: 94603
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PATENTIN DATA:
APPLICATION NUMBER: US/08/477,292
FILING DATE:
APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECOKET NUMBER: 36,373
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 36,373
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
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Conservative:
Mismatches:
Indels:
   Gaps:
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US-08-477-292-16
; Sequence 16, Application US/08477292
; Patent No. 6291641
  GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas
APPLICANT: McAree, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Tarbough, Patrice
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E
NUMBER OF SEQUENCES: 24
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   LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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548.00
100.00$
100.00$
83.16$
   INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
  Percent Similarity:
Best Local Similarity:
   HYPOTHETICAL: NORIGINAL SOURCE:
   Alignment Scores:
  US-08-477-292-16
   21
   Query Match:
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512.00
99.55%
99.55%
77.69%
; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-542-634-14
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
   APPLICANT: FLOETE, Thomas R.
APPLICANT: McAtee, C. Patrick
APPLICANT: Yarbough, Patrice O.
APPLICANT: Tarbough, Patrice O.
TITLE OF INVENTION: HEPATITIS E VIRUS ANY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
  AAGGTGGGTAAACTCGGGAGTTG 1977
  AFFLAL.
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
"FRIFPHONE: (415) 324-0880
   Sequence 14, Application US/08542634; Patent No. 6214970; GENERAL INFORMATION:
   TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 14:
   660 amino acids
  SEQUENCE CHARACTERISTICS:
   MOLECULE TYPE: protein HYPOTHETICAL: NO
   amino acid
   linear
  USA
  ORIGINAL SOURCE
   94306
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TOPOLOGY:
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   LENGIH:
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   US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-542-634-14 (1-660)
Hepatitis E Virus (Mexico Strain)
ORF-2
   660
658
0
  Conservative:
Mismatches:
   Length:
Matches:
   Indels:
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GENERAL INFORMATION:
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 31
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
   Conservative:
Mismatches:
Indels:
  Length:
Matches:
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
   TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 14:
   : 660 amino acids
amino acid
  512.00
99.55%
99.55%
77.69%
   SEQUENCE CHARACTERISTICS
  COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
   MOLECULE TYPE: protein HYPOTHETICAL: NO
   INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
  linear
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1977 G 1977
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  Alignment Scores:
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  US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-259-148A-18 (1-435)
   APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
   435
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  COMPUTER ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
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COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-ANN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-ANN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-ANN-1992
RIUNG DATE: 13-ANN-1992
APPLICATION NUMBER: US 420,921
FILING DATE: 13-ANN-1992
APPLICATION NUMBER: US 420,921
  Conservative:
Mismatches:
Indels:
   APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNM-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REPRENCE/DOCKET NUMBER: 4600-0093.20
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROM: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
   Length:
Matches:
  STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA
   C2, MEXICO, FIGURE
  APPLICATION NUMBER: US 367,486 FILING DATE: 16-JUN-1989 PRIOR APPLICATION DATA:
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
   435.00
100.00%
100.00%
66.01%
  LENGTH: 435 amino acids
   MOLECULE TYPE: protein HYPOTHETICAL: NO
   FILING DATE: 13-OCT-7
PRIOR APPLICATION DATA:
  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
   amino acid
  linear
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   USA
  94306
  HYPOTHETICAL:
   ;
US-08-259-148A-18
  Alignment Scores:
Pred. No.:
  TOPOLOGY:
APPLICANT:
APPLICANT:
APPLICANT:
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   Score:
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1572

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1632

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361

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8

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1392

240

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Query Match:
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   401 PheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAla 420
1873 TICTGCCCTGAATGCCGCGCTTTAAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCT
   Sequence 18, Application US/08484054
; Patent No. 5776689
; GENERAL INFORMATION:
APPLICANT: Bradey, Daniel W.
APPLICANT: Twu, Ur-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jabert W.
APPLICANT: Tam, Abert W.
APPLICANT: Tam, Abert W.
APPLICANT: Tam, Heptiis B Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADRRESS:
   1933 GAGCTCCAGCCCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1977
   421 GluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 435
  COUNTY:

ZIP: 94306
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
WILING DATE: 07-UIN-1995
   ...urkESSEE: Dehlinger & Associates
CITY: 350 Cambridge Avenue, Suite 250
CITY: CA
   4600-0093.38
  PILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING APPLICATION DATA:
APPLICATION NUMBER: US 420,921
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APPLICATION NUMBER: US 336,672
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
  REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
  NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
  SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
   RESULT 12
US-08-484-054-18
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   201 AlalleProHisAspIleAspLeuGlyAspSerArgValVallleGlnAspTyrAspAsn 220
  221 GlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeu 240
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  161 GluLeuileSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsn
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  1033 GCCACCAGGITCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGC
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  1213 GGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTT
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   US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-484-054-18 (1-435)
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   Conservative:
Mismatches:
Indels:
   C2, MEXICO, FIGURE 9
   Length:
Matches:
  435.00
100.00%
100.00%
66.01%
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
  ; INDIVIDUAL ISOLATE:
US-08-484-054-18
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DB:
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   CICCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCTTCGTGGCAAGCTC 1632
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   1933 GAGCICCAGCGCCTIAAAGIIAAGGIGGGIAAAACICGGGAGIIG 1977
  APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Micchell, Carl
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01.MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
   US-07-876-941A-18
; Sequence 18, Application US/07876941A
; Patent No. 5885768
; GENERAL INFORMATION:
   APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
   FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
  CITY: Palo Alto
STATE: CA
  USA
  COUNTRY:
 1513
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   1813
   421
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Conservative:
Mismatches:
   FILING DATE: 17-UWE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELECOMMUNICATION INFORMATION:
TELEFAON: (415) 324-0880
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                 FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
    US 336,672
  TYPE: amino acids
TOPOLOGY: li-
  435.00
100.00%
100.00%
66.01%
  MOLECULE TYPE: protein HYPOTHETICAL: NO
   ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
APPLICATION NUMBER:
   Best Local Similarity:
  Percent Similarity:
  US-07-876-941A-18
   Alignment Scores:
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973 AGCACTGCTCGTCACTCCGCCCGAGGGCCGACGGGACTGCGAGCTGACCACACTGCA 1032
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Indels:
   Length:
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  4600-0093.30
      APPLICATION NUMBER: US/07/870,985A
CLASSIPICATION NUMBER: US/07/870,985A
CLASSIPICATION 1435
FILING DATE: 20-APRIL-1992
FILING DATE: 17-JAN-1992
FILING DATE: 17-JAN-1992
FILING DATE: 05-APRIL-1990
FILING DATE: 05-APRIL-1990
FILING DATE: 13-CCTOBER-1989
FILING DATE: 13-CCTOBER-1989
FILING DATE: 14-JUNE-1989
FILING DATE: 16-JUNE-1989
FILING DATE: 16-JUNE-1989
FILING DATE: 16-JUNE-1989
FILING DATE: 11-APRIL-1989
FILING DATE: 11-APRIL-1988
ATTORNEYA AGENT INFORMATION:
WANNEY: PARKET DATE: 17-JUNE-1988
ATTORNEYA CASEN TROORMATION:
  Gaps:
   NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INPORMATION:
TELEPRONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
   435.00
100.00%
100.00%
66.01%
   435 amino acids
  MOLECULE TYPE: protein HYPOTHETICAL: NO
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US-07-870-985A-18
  amino acid
  linear
   Percent Similarity:
Best Local Similarity:
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   Alignment Scores:
  TOPOLOGY:
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  913
  733
   853
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DB:
   Pred. No.:
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   US-07-870-985A-18

Sequence 18, Application US/07870985A

Fatent No. 6455492

GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Twu, Jr.Shinel W.
APPLICANT: Twu, Jr.Shinel W.
APPLICANT: Twu, Jr.Shinel R.
APPLICANT: Twu, Jr.Shinel R.
APPLICANT: Twu, Jr.Shinel R.
APPLICANT: Twu, Jr.Shinel R.
APPLICANT: Two, Jr.Shinel R.
APPLICANT: Tam, Albert W.
IAPPLICANT: Tam, Albert W.
IAPPLICANT: Tam, Albert W.
CAPPLICANT: TAM, Albert W.
INTILE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
  1933 GAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1977
   GluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 435
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
  STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
   USA
   94306
  COUNTRY:
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  1153
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Sequence 16, Application US/08542634
Patent No. 6214970
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: Moace, C. Patrick
APPLICANT: Yarbough, Patrice O.

RESULT 15 US-08-542-634-16

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   514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT
   APPLICANT: Zhang, Yifan
TITE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
   US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-542-634-16 (1-549)
   Hepatitis E virus (Mexico strain)
r62kba, FIGURE 4
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1
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
  Length:
Matches:
Conservative:
  Mismatches:
  ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0800
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
  Indels:
  E: Dehlinger & Associates
350 Cambridge Ave., Suite 250
  : 549 amino acids
amino acid
  401.00
99.45%
99.45%
60.85%
  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
  single
   INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
  Percent Similarity:
Best Local Similarity:
  Palo Alto
   STRANDEDNESS:
  USA
  ADDRESSEE:
STREET: 35C
CITY: Palo
   Alignment Scores:
Pred. No.:
   US-08-542-634-16
  STATE: C. COUNTRY:
  LENGTH:
   634
   Query Match
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|-----|-----------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------|-----|--|
| 480 | 1830                                                                  | 200                                                                  | 1890                                                               | 520                                                                  | 1950                                   | 540 |  |
| ДD  | ολ                                                                    | qq                                                                   | ò                                                                  | qq                                                                   | ò                                      | qu  |  |